

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 3 11:19:37 1998; MasPar time 2.63 Seconds
 Tabular output not generated. 58.067 Million cell updates/sec

Title: >US-08-137-117D-117
 Description: (1-11) from US08137117D.pep
 Perfect Score: 70
 Sequence: 1 RASQDISSYLN 11

Scoring table: PAM 150
Gap 15

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-gensseq30
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 17.502; Variance 52.635; scale 0.333

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	70	100.0	126	5	R29015	4.74e-01
2	70	100.0	126	5	R29013	4.74e-01
3	70	100.0	127	5	R28670	4.74e-01
4	67	95.7	108	20	W00834	1.05e+00
5	67	95.7	108	20	W04177	1.05e+00
6	67	95.7	109	17	R52039	1.05e+00
7	67	95.7	127	22	W11815	1.05e+00
8	67	95.7	127	22	W11817	1.05e+00
9	67	95.7	127	5	R29010	1.05e+00
10	67	95.7	131	14	R84553	1.05e+00
11	67	95.7	268	8	R44226	1.05e+00
12	67	95.7	273	9	R52865	1.05e+00
13	66	94.3	128	5	R09426	1.37e+00
14	66	94.3	128	19	W06215	1.37e+00
15	64	91.4	11	20	W13920	2.31e+00
16	64	91.4	95	12	R20258	2.31e+00
17	64	91.4	95	12	R27065	2.31e+00
18	64	91.4	107	10	R54260	2.31e+00
19	64	91.4	107	19	W01284	2.31e+00
20	64	91.4	107	19	W01283	2.31e+00

21 64 91.4 107 10 R54261 Anti-HIV gp120 immuno 2.31e+00
 22 64 91.4 108 23 W13521 Anti-melanoma light c 2.31e+00
 23 64 91.4 108 23 W13530 Anti-melanoma light c 2.31e+00
 24 64 91.4 113 20 W13524 Light chain #2 for an 2.31e+00
 25 64 91.4 114 20 W13922 Light chain #1 for an 2.31e+00
 26 64 91.4 127 7 R39265 Mouse C4G1 Ig light-c 2.31e+00
 27 64 91.4 132 22 W2842 Human anti-tumour ant 2.31e+00
 28 64 91.4 214 6 R30776 H52L6-158 murine anti 2.31e+00
 29 64 91.4 214 7 R43338 Completely humanised 2.31e+00
 30 64 91.4 214 19 W00373 Anti-CD18 chimeric an 2.31e+00
 31 64 91.4 233 6 R30777 pH52-9.0 humanised mu 2.31e+00
 32 63 90.0 104 19 W01285 VL region of HIV neut 3.00e+00
 33 63 90.0 104 9 R54318 Anti-HIV gp120 immuno 3.00e+00
 34 63 90.0 107 7 R41283 Moderate-risk modifie 3.00e+00
 35 63 90.0 107 7 R38614 Low-risk modified pr 3.00e+00
 36 63 90.0 109 6 R30764 Consensus humanised a 3.00e+00
 37 63 90.0 109 9 R47041 Sequence of the conse 3.00e+00
 38 63 90.0 127 19 R99003 MAB VL17E5 light chai 3.00e+00
 39 62 88.6 11 17 R52523 Gloop-2 light chain c 3.89e+00
 40 62 88.6 104 9 R54322 Anti-HIV gp120 immuno 3.89e+00
 41 62 88.6 107 6 R30769 huxCD3v9, humanised m 3.89e+00
 42 62 88.6 107 6 R30768 Murine anti-CD3 MAB U 3.89e+00
 43 62 88.6 108 4 R21286 Murine VL kappa group 3.89e+00
 44 62 88.6 108 10 R54062 Anti-cancer monoclonal 3.89e+00
 45 62 88.6 128 5 R29579 CLN-IgG kappa. 3.89e+00

ALIGNMENTS

RESULT 1
 ID R29015 standard; Protein; 126 AA.
 AC R29015;
 DT 30-MAR-1993 (first entry)
 DE PUC-RV1-PM1a.
 KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;
 KW complementarity determining region; mouse; monoclonal; hybridoma;
 KW plasmid; polymerase chain reaction; amplify.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "Leader peptide"
 FT Region 20..42
 FT /label= FR1
 FT Region 43..53
 FT /label= CDR1
 FT Region 54..68
 FT /label= FR2
 FT Region 69..75
 FT /label= CDR2
 FT Region 76..107
 FT /label= FR3
 FT Region 108..116
 FT /label= CDR3
 FT Region 117..126
 FT /label= FR4
 FT WO9219759-A.
 PD 12-NOV-1992.
 PD 24-APR-1992; J00544.
 PR 25-APR-1991; JP-095476.
 PR 19-FEB-1992; JP-032084.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
 WPI; 92-398882/48.
 DR N-PSDB; Q31366.
 DR Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 PS Disclosure; Page 144-5; 207pp; Japanese.
 CC The sequences given in R29012-15 are portions of monoclonal antibodies
 CC which were encoded by plasmids derived from mouse hybridomas. The DNA
 CC encoding complementarity determining regions (CDR's) was isolated by
 CC polymerase chain reaction. These antibodies recognise human
 CC interleukin-6 receptor (IL-6R). The mouse hybridoma cells were

CC transformed with the plasmids encoding these genes which caused the
 CC secretion of these antibodies from the hybridoma cells.
 SQ Sequence 126 AA;

Query Match 100.0%; Score 70; DB 5; Length 126;
 Best Local Similarity 100.0%; Pred. No. 4.74e-01;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 rasqdisssyn 53
 |||||
 QY 1 RASQDISSYN 11

RESULT 2

ID R29013 standard; Protein; 126 AA.

AC R29013;

DT 30-MAR-1993 (first entry)

DE pUC-RVH-PM1a.

KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;

KW complementarity determining region; mouse; monoclonal; hybridoma;

KW plasmid; polymerase chain reaction; amplify.

OS Synthetic.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /note= "Leader peptide"

FT Region 20..42

FT /label= FR1

FT Region 43..53

FT /label= CDR1

FT Region 54..68

FT /label= FR2

FT Region 69..75

FT /label= CDR2

FT Region 76..107

FT /label= FR3

FT Region 108..116

FT /label= CDR3

FT Region 117..126

FT /label= FR4

PN WO9219759-A.

PD 12-NOV-1992.

PF 24-APR-1992; J00544.

PR 25-APR-1991; JP-095476.

PR 19-FEB-1992; JP-032084.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;

DR WPI; 92-398882/48.

DR N-PSDB; Q31361.

PT Reconstituted human antibody to human interleukin-6 receptor -

PT has low antigenicity and contains mouse V-region complementarity

PT determining regions

PS Disclosure; Page 140-1; 207pp; Japanese.

CC The sequences given in R29012-15 are portions of monoclonal antibodies

CC which were encoded by plasmids derived from mouse hybridomas. The DNA

CC encoding complementarity determining regions (CDR's) was isolated by

CC polymerase chain reaction. These antibodies recognise human

CC interleukin-6 receptor (IL-6R). The mouse hybridoma cells were

CC transformed with the plasmids encoding these genes which caused the

CC secretion of these antibodies from the hybridoma cells.

SQ Sequence 126 AA;

Query Match 100.0%; Score 70; DB 5; Length 126;
 Best Local Similarity 100.0%; Pred. No. 4.74e-01;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 rasqdisssyn 53

|||||

QY 1 RASQDISSYN 11

RESULT 3

ID R28670 standard; Protein; 127 AA.

AC R28670;

DT 30-MAR-1993 (first entry)
 DE pPM-k3 protein product.
 KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
 KW heavy chain; variable region; mouse; monoclonal; hybridoma; PMI;
 KW plasmid; pPM-k3; pPM-h1.
 OS Synthetic.

FH Key Location/Qualifiers

FT Peptide 1..20

FT /note= "Signal peptide"

FT Protein 21..127

FT /note= "Mature peptide"

PN WO9219759-A.

PD 12-NOV-1992.

PF 24-APR-1992; J00544.

PR 25-APR-1991; JP-095476.

PR 19-FEB-1992; JP-032084.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;

DR WPI; 92-398882/48.

DR N-PSDB; Q30755.

PT Reconstituted human antibody to human interleukin-6 receptor -

PT has low antigenicity and contains mouse V-region complementarity

PT determining regions

PS Disclosure; Page 121-122; 207pp; Japanese.

CC The sequences given in R28670-71 were encoded by plasmids which were

CC used in example to illustrate the production of a human antibody which

CC recognises human interleukin-6 receptor (IL-6R). The antibody

CC comprises light (L) chain and heavy (H) chain variable regions which

CC were derived from a mouse monoclonal antibody produced from the

CC hybridoma PMI which contained the plasmids pPM-k3 and pPM-h1.

SQ Sequence 127 AA;

Query Match 100.0%; Score 70; DB 5; Length 127;
 Best Local Similarity 100.0%; Pred. No. 4.74e-01;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 44 rasqdisssyn 54

|||||

QY 1 RASQDISSYN 11

RESULT 4

ID W00834 standard; Protein; 108 AA.

AC W00834;

DT 20-MAY-1997 (first entry)

DE Variable light chain of anti-human Fas ligand antibody NOK-1.

KW Variable region; light chain; human; Fas ligand; monoclonal;

KW antibody; NOK-1; hybridoma; inhibition; apoptosis; assay;

KW diagnosis; disease; hepatitis; infectious mononucleosis;

KW systemic lupus erythematosus.

OS Mus musculus.

PN W09629350-A1.

PD 26-SEP-1996.

PF 21-MAR-1996; J00734.

PR 20-MAR-1995; JP-087420.

PR 27-OCT-1995; JP-303492.

PA (SUME) SUMITOMO ELECTRIC IND CO.

PI Kayagaki N, Nakata M, Okumura K, Yagita H;

DR WPI; 96-443140/44.

DR N-PSDB; T39560.

PT Monoclonal antibody specifically recognising the Fas ligand - useful

PT for the detection of Fas ligands either on cell surface or in

PT solution

PS Claim 41; Pages 93-94; 133pp; Japanese.

CC The present sequence is the light chain variable region of the

CC anti-human Fas ligand monoclonal antibody (MAB) NOK-1. NOK-1 is

CC produced by the hybridoma NOK-1 (FERM BP-5044), which was prepared

CC by immunising mice with transformed human Fas ligand expressing COS

CC cells, and fusing spleen cells isolated from the mice with myeloma

CC P3x6Ag8.53 (ATCC CRL-1580) cells. The MAB recognises the human

CC Fas ligand on the cell surface or in solution, and can be used to

CC inhibit the apoptosis inducing cell surface Fas ligand/Fas

CC reaction. The MAB can also be used for a Fas ligand assay in

CC biological samples (e.g. human blood), especially for disease
 CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic
 CC lupus erythematosus.
 SQ Sequence 108 AA;

Query Match 95.7%; Score 67; DB 20; Length 108;
 Best Local Similarity 90.9%; Pred. No. 1.05e+00;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnynl 34
 |||||:||||
 QY 1 RASQDISSYLN 11

RESULT 5

ID W04177 standard; Protein; 108 AA.
 AC W04177;
 DT 19-MAY-1997 (first entry)
 DE Variant variable light chain of Fas ligand antibody NOK-1.
 KW Variable region; light chain; human; Fas ligand; monoclonal;
 KW antibody; NOK-1; hybridoma; inhibition; apoptosis; assay;
 KW diagnosis; disease; hepatitis; infectious mononucleosis;
 KW systemic lupus erythematosus; variant.
 OS Mus musculus.
 PN W09629350-A1.
 PD 26-SEP-1996; J00734.
 PF 21-MAR-1996;
 PR 20-MAR-1995; JP-087420.
 PR 27-OCT-1995; JP-303492.
 PA (SUME) SUMITOMO ELECTRIC IND CO.
 PI Kayagaki N, Nakata M, Okumura K, Yagita H;
 DR WPI: 96-443140/44.
 DR N-PSDB; T39550.
 PT Monoclonal antibody specifically recognising the Fas ligand - useful
 PT for the detection of Fas ligands either on cell surface or in
 PT solution
 PS Claim 20; Pages 80-81; 133pp; Japanese.
 CC The present sequence is a variant light chain variable region
 CC of the anti-human Fas ligand monoclonal antibody (WAB) NOK-1.
 CC is produced by the hybridoma NOK-1 (FERM BP-5044), which was
 CC prepared by immunising mice with transformed human Fas ligand
 CC expressing COS cells, and fusing spleen cells isolated from the
 CC mice with myeloma P3x63Ag8.653 (ATCC CRL-1580) cells. The MAB
 CC recognises the human Fas ligand on the cell surface or in solution,
 CC and can be used to inhibit the apoptosis inducing cell surface Fas
 CC ligand/Fas reaction. The MAB can also be used for a Fas ligand
 CC assay in biological samples (e.g. human blood), especially for
 CC disease diagnosis, e.g. hepatitis, infectious mononucleosis and
 CC systemic lupus erythematosus.
 SQ Sequence 108 AA;

Query Match 95.7%; Score 67; DB 20; Length 108;
 Best Local Similarity 90.9%; Pred. No. 1.05e+00;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnynl 34
 |||||:||||
 QY 1 RASQDISSYLN 11

RESULT 6

ID R52039 standard; Protein; 109 AA.
 AC R52039;
 DT 27-SEP-1996 (first entry)
 DE Light chain variable region of murine antibody lf19.
 KW antibody; humanised; murine; human; heavy chain; light; variable;
 KW framework region; complementarity determining region; reshaping;
 KW modelling; surface residue; modify.
 OS Mus sp.
 PN 1.23
 PF Key Location/Qualifiers
 PR Region 1..23
 FT /label= framework_region_1
 FT /note= "FR 1"

FT Region 24..34
 FT /label= complementarity_determining_region_1
 FT /note= "CDR 1"
 FT Region 35..49
 FT /label= FR_2
 FT Region 50..56
 FT /label= CDR_2
 FT Region 57..88
 FT /label= FR_3
 FT Region 89..97
 FT /label= CDR_3
 FT Region 98..109
 FT /label= FR_4
 PN EP-592106-A1.
 PD 13-APR-1994.
 PF 07-SEP-1993; 307051.
 PR 09-SEP-1992; US-942245.
 PA (PEDE/) PEDERSEN J T.
 PA (IMMU-) IMMUNOGEN INC.
 DR WPI: 94-120230/15.
 PT Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved
 PT therapeutic efficiency by presenting human surface on V-region
 PS Example 1; Fig 3A; 230pp; English.
 CC The present sequence is that of the light chain variable (LC VR) region
 CC of murine antibody lf19. This sequence was aligned with 11 other known
 CC antibody LC VRs and a set of framework positions of surface exposed amino
 CC acid residues was determined. This information can be used in a method to
 CC determine how to modify a rodent antibody or fragment by resurfacing in
 CC order to produce a humanised rodent antibody. Residues (determined from
 CC alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86,
 CC 87, 111, 115, 116 and 117 are accessible residues. None of the entire
 CC combinations of surface residues in the murine sequences were found in
 CC the human sequences and vice versa. However the residues in individual
 CC positions appear to be conserved.
 SQ Sequence 109 AA;

Query Match 95.7%; Score 67; DB 17; Length 109;
 Best Local Similarity 90.9%; Pred. No. 1.05e+00;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnynl 34
 |||||:||||
 QY 1 RASQDISSYLN 11

RESULT 7

ID W11815 standard; Protein; 127 AA.
 AC W11815;
 DT 20-OCT-1997 (first entry)
 DE Mouse anti-human Fas ligand antibody F919 light chain.
 KW Human; Fas ligand; antigen; neutral; antibody; apoptosis; HIV;
 KW induction; assay; enzyme linked immunosorbant assay; diagnosis;
 KW disease; hepatitis B; hepatitis C; human immunodeficiency virus;
 KW graft versus host disease; ulcerative colitis; sequelae;
 KW myocardial infarction; mouse; murine; monoclonal; treatment;
 KW complementarity determining region; CDR.
 OS Mus spp.
 PF Key Location/Qualifiers
 PR Region 44..54
 FT /label= CDR_1
 FT Region 70..76
 FT /label= CDR_2
 FT Region 109..117
 FT /label= CDR_3
 PN W09702290-A1.
 PD 23-JAN-1997.
 PF 01-JUL-1996; J01820.
 PR 17-MAY-1996; JP-649100.
 PR 30-JUN-1995; JP-188480.
 PA (MOCH) MOCHIDA PHARM CO LTD.
 PA (OSAB-) OSAKA BIOSCIENCE INST.

PI Co MS, Matsusue T, Nagata S, Shirakawa K, Vasquez M;
DR WPI: 97-108917/10.
DR N-PSDB: T59500.
PT Antibody reactive with Fas ligand capable of inducing apoptosis -
PT used for diagnostic assay of Fas ligand in body fluids and for
PT treatment of diseases in which Fas ligand/Fas antigen is involved
PS Claim 5; Fig 10; 164pp; Japanese.
CC The present sequence is the light chain of the mouse
CC anti-apoptosis inducing human Fas ligand, monoclonal antibody,
CC F919. The antibody can be used in a Fas ligand assay, e.g. an
CC enzyme linked immunosorbent assay, to diagnose diseases in which
CC the Fas ligand/Fas antigen system is implicated, e.g. hepatitis
CC B/C, human immunodeficiency virus, graft/host disorders,
CC ulcerative colitis or sequelae of myocardial infarction. The
CC antibody may also be used to treat such diseases.
SQ Sequence 127 AA;

Query Match 95.7%; Score 67; DB 22; Length 127;
Best Local Similarity 90.9%; Pred. No. 1.05e+00;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 44 rasqdisnyln 54
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 8
ID W11817 standard; Protein; 127 AA.

AC W11817;
DE Humanised mouse anti-human Fas ligand antibody F919 light chain.
KW Human; Fas ligand; antigen; neutral; antibody; apoptosis; HIV;
KW induction; assay; enzyme linked immunosorbent assay; diagnosis;
KW disease; hepatitis B; hepatitis C; human immunodeficiency virus;
KW graft versus host disease; ulcerative colitis; sequelae; chimeric;
KW myocardial infarction; mouse; murine; monoclonal; treatment.
OS Chimeric - Mus spp.
OS Chimeric - Homo sapiens.
OS Synthetic.

FH Key Location/Qualifiers
FT Region 44..54
FT /label= CDR_1 70..76
FT Region
FT /label= CDR_2 109..117
FT Region
FT /label= CDR_3
PN W09702290-A1.
PD 23-JAN-1997.
PF 01-JUL-1996; J01820.
PR 17-MAY-1996; US-649100.
PR 30-JUN-1995; JP-188480.

PA (MOCH) MOCHIDA PHARM CO LTD.
PI (OSAB-) OSAKA BIOSCIENCE INST.
PI Co MS, Matsusue T, Nagata S, Shirakawa K, Vasquez M;
DR WPI: 97-108917/10.
DR N-PSDB: T59502.
PT Antibody reactive with Fas ligand capable of inducing apoptosis -
PT used for diagnostic assay of Fas ligand in body fluids and for
PT treatment of diseases in which Fas ligand/Fas antigen is involved
PS Claim 5; Fig 12; 164pp; Japanese.
CC The present sequence is the light chain of the humanised
CC mouse anti-apoptosis inducing human Fas ligand, monoclonal
CC antibody, F919. The antibody can be used in a Fas ligand assay,
CC e.g. an enzyme linked immunosorbent assay, to diagnose diseases
CC in which the Fas ligand/Fas antigen system is implicated, e.g.
CC hepatitis B/C, human immunodeficiency virus, graft/host disorders,
CC ulcerative colitis or sequelae of myocardial infarction. The
CC antibody may also be used to treat such diseases.
SQ Sequence 127 AA;

Query Match 95.7%; Score 67; DB 22; Length 127;
Best Local Similarity 90.9%; Pred. No. 1.05e+00;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 44 rasqdisnyln 54
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 9

ID R29010 standard; Protein; 127 AA.
AC R29010; 1993 (first entry)
DE p146-k3 protein product.
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15;
KW plasmid; p146-k3; p146-h1.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "Signal peptide"
FT Protein 21..127
FT /note= "Mature peptide"
PN W09219759-A.
PD 12-NOV-1992.
PF 24-APR-1992; J00544.
PR 25-APR-1991; JP-095476.
PR 19-FEB-1992; JP-032084.
PA (CHUS) CHUGAI SEIYAKU KK.
PI Bendig MW, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WPI: 92-398882/48.
DR N-PSDB: Q30759.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PS Disclosure; Page 127-128; 207pp; Japanese.
CC The sequences given in R29010-11 were encoded by plasmids which were
CC used in example to illustrate the production of a human antibody which
CC recognises human interleukin-6 receptor (IL-6R). The antibody
CC comprises light (L) chain and heavy (H) chain variable regions which
CC were derived from a mouse monoclonal antibody produced from the
CC hybridoma AUK146-15 which contained the plasmids p146-k3 and p146-h1.
SQ Sequence 127 AA;

Query Match 95.7%; Score 67; DB 5; Length 127;
Best Local Similarity 90.9%; Pred. No. 1.05e+00;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 44 rasqdisnyln 54
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 10
ID R84553 standard; Protein; 131 AA.

AC R84553;
DR 02-FEB-1996 (first entry)
DE MAB SCH94.03 light chain.
KW Monoclonal antibody; MAB; SCH94.03; hybridoma; central nervous system;
KW CNS; demyelination; multiple sclerosis; neural disease; therapeutic.
OS Mus sp.

FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Leader_peptide
FT Region 44..54
FT /label= CDR1 70..76
FT Region
FT /label= CDR2 109..117
FT Region
FT /label= CDR3 116..128
FT /label= Joining_region
FT Region 129..131
FT /label= C-kappa_region
PN W09530004-A1.
PD 09-NOV-1995.

PF 27-APR-1995; U05262.
PR 29-APR-1994; US-236520.
PA (MAYO-) MAYO FOUNDATION.
PI Miller DJ, Rodriguez M;
WPI: 95-393077/50.
DR N-PSDB; T05311.
PT Monoclonal antibodies which stimulate central nervous system
PT re-myelination - are produced by hybridoma ATCC CRL 11627, for
PT treating multiple sclerosis, and viral or post-neural diseases of
PT the CNS.
PS Disclosure; Page 36-37; 63pp; English.
CC Hybridoma ATCC CRL 11627 was obtd. from a SJL/J mouse injected with
CC spinal cord homogenate from a mammal uninfected with any
CC demyelinating disease. The hybridoma produced a monoclonal antibody
CC (SCH94.03) useful in promoting CNS remyelination. The SCH94.03
CC light chain amino acid sequence is given in R84553.
SQ Sequence 131 AA;

Query Match 95.7%; Score 67; DB 14; Length 131;
Best Local Similarity 90.9%; Pred. No. 1.05e+00;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 44 rasqdisnyln 54
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 11
ID R44226 standard; protein; 268 AA.
AC R44226;
DT 10-JUN-1994 (first entry)
DE Chimeric Ig superfamily protein analogue R19(D1.3).
KW CHI-protein; Immunoglobulin superfamily; multivalent antigen binding;
KW engineered fusion protein; beta-barrel domain; chimaeric;
KW complementarity determining region; cell imaging; targetting.
OS Synthetic.
FH Key Location/Qualifiers
FT Region 1..30
FT /label= H_FR1
FT /note= "Heavy chain framework region from R19.9"
FT Region 31..35
FT /label= H1
FT /note= "Primary CDR loop from R19.9"
FT Region 36..39
FT /label= FR2A
FT /note= "Heavy chain framework region from R19.9"
FT Region 40..45
FT /label= H3'
FT /note= "CDR loop spliced into chi-site from D1.3"
FT Region 46..48
FT /label= FR2B
FT /note= "Heavy chain framework region from R19.9"
FT Region 49..65
FT /label= H2
FT /note= "Primary CDR loop from R19.9"
FT Region 66..89
FT /label= H_FR3A
FT /note= "Heavy chain framework region from R19.9"
FT Region 90..92
FT /label= H1'
FT /note= "CDR loop spliced into chi-site from D1.3"
FT Region 93..97
FT /label= H_FR3B
FT /note= "Heavy chain framework region from R19.9"
FT Region 98..112
FT /label= H3
FT /note= "Primary CDR loop from R19.9"
FT Region 113..116
FT /label= H_FR4
FT /note= "Heavy chain framework region from R19.9"
FT Region 117..135
FT /label= H2'
FT /note= "CDR loop spliced into chi-site from D1.3"

FT Region 136..155
FT /note= "bridge/linker"
FT Region 156..178
FT /label= L_FR1
FT /note= "Light chain framework region from R19.9"
FT Region 179..189
FT /label= L1
FT /note= "Primary CDR loop from R19.9"
FT Region 190..193
FT /label= FR2A
FT /note= "Light chain framework region from R19.9"
FT Region 194..199
FT /label= L3'
FT /note= "CDR loop spliced into chi-site from D1.3"
FT Region 200..203
FT /label= FR2B
FT /note= "Light chain framework region from R19.9"
FT Region 204..210
FT /label= L2
FT /note= "Primary CDR loop from R19.9"
FT Region 211..237
FT /label= L_FR3A
FT /note= "Light chain framework region from R19.9"
FT Region 238..241
FT /label= L1'
FT /note= "CDR loop spliced into chi-site from D1.3"
FT Region 242..244
FT /label= FR3B
FT /note= "Light chain framework region from R19.9"
FT Region 245..253
FT /label= L3
FT /note= "Primary CDR loop from R19.9"
FT Region 254..255
FT /label= FR4
FT /note= "Light chain framework region from R19.9"
FT Region 256..268
FT /label= L2'
FT /note= "CDR loop spliced into chi-site from D1.3"
FT W09323357-A.
PN 25-NOV-1993.
PD 07-MAY-1993; U04338.
PR 08-MAY-1992; US-881109.
PA (CREA-) CREATIVE BIOMOLECULES.
PI Huston JS, Keck PC;
DR WPI: 93-386569/48.
PT Chimeric multivalent protein analogues - useful for diagnostic
PT imaging and cytotoxic therapy.
PS Example 1; Fig 14; 106pp; English.
CC This sequence is an example of a CHI-protein constructed according
CC to the invention. The novel CHI (Chimeric Immunoglobulin)-proteins
CC are comprised of at least 1 beta-barrel forming domain. The antigen
CC binding sites of the molecule are located in the beta-barrel
CC domain(s). Splice sites for insertion of specific binding sites are
CC located by computer comparisons of homology and structure. Depending
CC on the ligand binding specificity of the chimeric molecules, they
CC can be targetted for imaging, irradiating or delivering cytotoxic
CC substances to specific tissues.
SQ Sequence 268 AA;

Query Match 95.7%; Score 67; DB 8; Length 268;
Best Local Similarity 90.9%; Pred. No. 1.05e+00;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 179 rasqdisnyln 189
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 12
ID R52865 standard; Protein; 273 AA.
AC R52865;
DT 09-SEP-1994 (first entry)
DE Anti-influenza N10 scFv.

KW Monoclonal antibody N10; target binding polypeptide; scFv;
 KW scFv; single chain antibody; protein secretion; FLAG;
 KW Escherichia coli; antibody engineering; humanized antibody;
 KW Influenza virus; neuraminidase.
 OS Not specified.

FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /label- Sig_peptide
 FT Peptide 266..273
 FT /note= "C-terminal FLAG tail"
 PN W09407921-A.
 PD 14-APR-1994.
 PF 24-SEP-1993; AU0491.
 PR 25-SEP-1992; AU-004973.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PI Atwell JL, Colman PM, Hudson PJ, Irving RA, Kortt A;
 PI Lah M, Malbyrl, Power BE;
 DR WPI: 94-135515/16.
 DR P-PSDB: Q62957.
 PT New target-binding polypeptide(s) used for diagnosis, etc. -
 PT having a stable core polypeptide region with at least one
 PT target-binding region covalently attached, opt. mutated to alter
 PT specificity, etc.
 PS Disclosure: Page 41; 67pp; English.
 CC An scFv fragment of NC10 (a monoclonal antibody that recognises
 CC influenza virus N9 neuraminidase) was expressed in Escherichia
 CC coli. The N-terminal PelB signal peptide directed the scFv
 CC fragment into the periplasm where it became associated with the
 CC insoluble membrane fraction. An octapeptide FLAG tail was fused to
 CC the C-terminus of scFv and used to monitor scFv during
 CC purification.
 SQ Sequence 273 AA;

Query Match 95.7%; Score 67; DB 9; Length 273;
 Best Local Similarity 90.9%; Pred. No. 1.05e+00;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 182 rasqdislyln 192
 QY 1 RASQDISSYLN 11

RESULT 13
 ID R09426 standard; Protein; 128 AA.
 AC R09426;
 DT 04-MAR-1993 (first entry)
 DE ME4 Light Chain V Region (mouse).
 KW Monoclonal antibody; chimera; light; heavy; chain; constant;
 KW variable; antigen; diagnosis; cancer; tumour.
 OS Mus musculus.
 PN W09002569-A.
 PD 22-MAR-1990.
 PF 06-SEP-1989; U03852.
 PR 06-SEP-1988; US-240624.
 PR 08-SEP-1988; US-241744.
 PR 13-SEP-1988; US-243739.
 PR 04-OCT-1988; US-253002.
 PR 19-JUN-1989; US-367641.
 PR 21-JUL-1989; US-382768.
 PI (ITGE-) INT GENETIC ENG INC.
 PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
 DR WPI: 90-115825/15.
 DR N-PSDB: Q08608.

PT Chimeric mouse-human antibodies - prepd. using genes coding for
 PT constant human region murine variable region, esp. to 3 tumour
 PT antigen
 PS Claim 13; Page 123 + Fig 29; 173pp; English.
 CC The sequence is used in the prodn. of a chimeric antibody mol.
 CC comprising two light chains and two heavy chains, each having a
 CC constant region (human) and a variable region (murine) having
 CC specificity to an antigen bound by murine monoclonal antibody
 CC (MAB) ME4. The chimeric antibodies can be used for any purpose for
 CC which the original murine MABs can be used, with the advantage that

CC they are more compatible with the human body. They are esp. used for
 CC the diagnosis and treatment of cancer.
 SQ Sequence 128 AA;

Query Match 94.3%; Score 66; DB 5; Length 128;
 Best Local Similarity 81.8%; Pred. No. 1.37e+00;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 44 rasqdittlyln 54
 QY 1 RASQDISSYLN 11

RESULT 14
 ID W06215 standard; Protein; 128 AA.
 AC W06215;
 DT 13-FEB-1997 (first entry)
 DE MAB ME4 light chain variable region.
 KW Chimeric antibody; monoclonal antibody; ME4; antibody engineering;
 KW tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;
 KW ovary carcinoma; melanoma; cancer; diagnosis; therapy; light chain.
 OS Mus sp.
 PN US5576184-A.
 PD 19-NOV-1996.
 PF 06-SEP-1988; 240624.
 PR 06-SEP-1988; US-240624.
 PR 08-SEP-1988; US-241744.
 PR 13-SEP-1988; US-243739.
 PR 04-OCT-1988; US-253002.
 PR 19-JUN-1989; US-367641.
 PR 21-JUL-1989; US-382768.
 PR 06-MAY-1991; US-659401.
 PR 27-DEC-1994; US-364001.
 PA (XOMA) XOMA CORP.
 PI Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
 DR WPI: 97-011249/01.
 DR N-PSDB: T43440.

PT Chimeric mouse-human antibodies - recognise a human tumour antigen,
 PT used for the treatment and diagnosis of human cancers
 PS Example 3; Fig 29; 102pp; English.
 CC The light chain variable region (W06215) of mouse monoclonal
 CC antibody ME4 is the product of a cDNA clone (T43440) isolated
 CC from a ME4 hybridoma cDNA library. MAB ME4 (IgG1) binds to an
 CC antigen that is expressed on the surface of human lung, breast,
 CC colon and ovary carcinomas and melanomas, but not on most normal
 CC adult tissues. The light chain and heavy chain variable regions
 CC (see also W06216) of ME4 can be linked to human constant regions
 CC and expressed in transformed host cells. Novel mouse-human
 CC chimeric antibodies (see also W06209-14 and W06217-18) can be
 CC produced that have specificity to human tumour antigens for use in
 CC the treatment and diagnosis of human cancer.
 SQ Sequence 128 AA;

Query Match 94.3%; Score 66; DB 19; Length 128;
 Best Local Similarity 81.8%; Pred. No. 1.37e+00;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 44 rasqdittlyln 54
 QY 1 RASQDISSYLN 11

RESULT 15
 ID W13920 standard; peptide; 11 AA.
 AC W13920;
 DT 15-MAY-1997 (first entry)
 DE Fragment of CDR-1 of light-chain variable region.
 KW Antibody; heavy chain; light chain; variable region; human; monoclonal;
 KW complementarity determining region; human; adr type hepatitis B virus;
 KW HB virus; CDR; virus antigen; anti-HB antibody; vaccine.
 OS Homo sapiens.
 PN J09020798-A.
 PD 21-JAN-1997.

PF 11-JUL-1995; 174752.
 PR 11-JUL-1995; JP-174752.
 PA (ASAH) ASAH KASEI KOGYO KK.
 DR WPI: 97-140911/13.
 DR N-PSDB; T60115.
 PT Human anti-Hepatitis B antibody - used in a adr type HB virus
 PT vaccine
 PS Claim 6; Page 2; 20pp; Japanese.
 CC This sequence represents a fragment of the complementarity determining
 CC region-1 (CDR-1) of the light chain variable region of a human
 CC monoclonal antibody of the invention. The antibody of the invention also
 CC contains the represented by W13912 in the CDR-1 of the heavy chain
 CC variable region. The antibody is capable of binding to adr type
 CC hepatitis B (HB) virus antigen. A human anti-HB virus monoclonal
 CC antibody preparation which is highly safe and is effective to adr type HB
 CC virus can be provided, using the monoclonal antibody. It can also be
 CC used as a vaccine against HB infection.
 SQ Sequence 11 AA;

Query Match 91.4%; Score 64; DB 20; Length 11;
 Best Local Similarity 90.9%; Pred. No. 2.31e+00;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 rasgsissyln 11
 |||| |||||
 Qy 1 RASQDISSYLN 11

Search completed: Tue Mar 3 11:19:50 1998
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W P E L L (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Mar 3 11:19:07 1998; Maspar time 2.96 Seconds
Tabular output not generated.
113.234 Million cell updates/sec
Title: >US-08-137-117D-117
Description: (1-11) from US08137117D.pep
Perfect Score: 70
Sequence: 1 RASQDISSYLN 11

Scoring table: PAM 150
Gap 15
Searched: 95051 seqs, 30469580 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: pirs3
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unann11 16:unann12 17:unann13
18:unrev

Statistics: Mean 23.804; Variance 32.457; scale 0.733
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length DB	ID	Description	Pred. No.	
1	68	97.1	105	7	PH0087	Ig kappa chain V reg	3.54e-03
2	67	95.7	93	7	S38564	Ig light chain V reg	5.82e-03
3	67	95.7	107	7	S69906	Ig kappa light chain	5.82e-03
4	67	95.7	107	7	B28044	Ig kappa chain V reg	5.82e-03
5	67	95.7	107	7	B28026	Ig kappa chain V reg	5.82e-03
6	67	95.7	107	7	A28044	Ig kappa chain V reg	5.82e-03
7	67	95.7	107	7	D48677	Ig light chain V-J r	5.82e-03
8	67	95.7	107	7	S69901	Ig kappa light chain	5.82e-03
9	67	95.7	108	7	S38862	Ig kappa chain V reg	5.82e-03
10	67	95.7	108	7	S69902	Ig kappa light chain	5.82e-03
11	67	95.7	108	7	S69900	Ig kappa light chain	5.82e-03
12	67	95.7	108	2	KVMSAR	Ig kappa chain V reg	5.82e-03
13	67	95.7	108	7	C26405	Ig kappa chain V reg	5.82e-03
14	67	95.7	108	7	PL0282	Ig light chain V reg	5.82e-03
15	67	95.7	108	7	A53276	Ig kappa chain V reg	5.82e-03
16	67	95.7	115	7	JL0080	Ig light chain V reg	5.82e-03
17	67	95.7	128	7	A26406	Ig kappa chain V reg	5.82e-03
18	67	95.7	109	7	S31981	Ig kappa chain - hum	1.55e-02
19	65	92.9	109	7	S31981	Ig kappa chain V-reg	2.53e-02
20	64	91.4	86	7	S34086	Ig kappa chain V-reg	2.53e-02

21	64	91.4	87	7	S34083	Ig kappa chain V reg	2.53e-02
22	64	91.4	87	7	S34084	Ig kappa chain V reg	2.53e-02
23	64	91.4	88	7	S21522	Ig kappa chain V reg	2.53e-02
24	64	91.4	88	7	S21528	Ig kappa chain V reg	2.53e-02
25	64	91.4	92	7	D28840	Ig kappa chain V reg	2.53e-02
26	64	91.4	101	7	B28840	Ig kappa chain V reg	2.53e-02
27	64	91.4	101	7	C28840	Ig kappa chain V reg	2.53e-02
28	64	91.4	107	7	B48677	Ig light chain V-J r	2.53e-02
29	64	91.4	107	7	A48677	Ig light chain V-J r	2.53e-02
30	64	91.4	107	7	S32188	Ig kappa chain V reg	2.53e-02
31	64	91.4	107	7	C48677	Ig light chain V-J r	2.53e-02
32	64	91.4	107	7	S36264	Ig lambda chain V reg	2.53e-02
33	64	91.4	108	7	S44122	Ig kappa chain V reg	2.53e-02
34	64	91.4	108	7	S47182	Ig kappa chain - hum	2.53e-02
35	64	91.4	108	7	B26405	Ig kappa chain V reg	2.53e-02
36	64	91.4	108	7	B49047	IgM monoclonal stria	2.53e-02
37	64	91.4	116	7	A27594	Ig kappa chain V reg	2.53e-02
38	64	91.4	117	7	S24206	Ig kappa chain V reg	2.53e-02
39	64	91.4	117	7	S24209	Ig kappa chain V reg	2.53e-02
40	64	91.4	122	7	A29380	Ig kappa chain V reg	2.53e-02
41	64	91.4	123	7	S40331	Ig kappa chain - hum	2.53e-02
42	64	91.4	126	7	A34904	Ig kappa chain V reg	2.53e-02
43	63	90.0	108	2	K1HU00	Ig kappa chain V-I r	4.09e-02
44	62	88.6	98	7	PH1082	Ig light chain V reg	6.60e-02
45	62	88.6	109	7	S31998	Ig kappa chain - hum	6.60e-02

ALIGNMENTS

RESULT	1	PH0087	#type fragment	
ENTRY		Ig kappa chain V region (anti-cyclosporin C and D) - mouse		
TITLE		(fragment)		
ORGANISM		#formal_name Mus musculus #common_name house mouse		
DATE		15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 16-Aug-1996		
ACCESSIONS		PH0087		
REFERENCE		PH0087		
#authors		Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Koehler, H.P.; Quesniaux, V.F.J.; Van Regenmortel, M.H.V.		
#journal		Mol. Immunol. (1990) 27:1029-1038		
#title		Analysis of the structural diversity of monoclonal antibodies to cyclosporine.		
#cross-references		MUID:91042649		
#accession		PH0087		
#molecule_type		mRNA		
#residues		1-105	#label SCH	
CLASSIFICATION		#superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin		
KEYWORDS				
FEATURE				
24-34		#region complementarity-determining 1\		
50-56		#region complementarity-determining 2\		
89-97		#region complementarity-determining 3\		
SUMMARY		#length 105 #checksum 9783		
Query Match		97.1%; Score 68; DB 7; Length 105;		
Best Local Similarity		90.9%; Pred. No. 3.54e-03;		
Matches		10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Db	24	rasqdistyln 34		
Qy	1	RASQDISSYLN 11		
RESULT	2	S38564	#type fragment	
ENTRY		Ig light chain V region (ASWU1) - mouse (fragment)		
TITLE		#formal_name Mus musculus #common_name house mouse		
ORGANISM		06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-May-1997		
DATE		S38564		
ACCESSIONS		S38559		
REFERENCE		Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.		
#authors				

#submission submitted to the EMBL Data Library, September 1993
#description Molecular analysis of mercury-induced anti-nucleolar
antibodies in H-2s Mice.

#accession S38564
#status preliminary
#molecule_type mRNA
#residues 1-93 #label MON
#cross-references EMBL:X75105
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
SUMMARY #length 93 #checksum 1511

Query Match 95.7%; Score 67; DB 7; Length 93;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 3
ENTRY S69906 #type complete
TITLE Ig kappa light chain (clone KL4A1) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
09-May-1997

ACCESSIONS S69906
REFERENCE Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
#authors Immunology (1992) 75:116-121
#journal B-cell proliferation initiated by Ia cross-linking and
#title sustained by interleukins leads to class switching but not
somatic mutation in vitro.

#accession S69906
#status preliminary; translation not shown
#molecule_type DNA
#residues 1-107 #label WYS
#cross-references EMBL:X55047

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 107 #molecular-weight 11827 #checksum 7550

Query Match 95.7%; Score 67; DB 7; Length 107;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 4
ENTRY B28044 #type complete
TITLE Ig kappa chain V region (gp1) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-May-1989 #sequence_revision 19-May-1989 #text_change
16-Aug-1996

ACCESSIONS B28044
REFERENCE Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
#authors Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6244-6248
#journal Identity of the V-kappa-10-Ars-A gene segments of the A/J and
#title BALB/c strains.
#cross-references MUID:87317629

#accession B28044
#molecule_type mRNA

#residues 1-107 #label NEE
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 107 #molecular-weight 11738 #checksum 7011

Query Match 95.7%; Score 67; DB 7; Length 107;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 24 rasqdisnyln 34
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 5
ENTRY B49026 #type complete
TITLE Ig kappa chain V region, anti-idiotypic monoclonal antibody -
mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
25-Oct-1996

ACCESSIONS B49026; PL0220
REFERENCE A49026

#authors Koizumi, T.; Puccetti, A.; Migliorini, P.; Barrett, K.J.;
Schwartz, R.S.
#journal Eur. J. Immunol. (1991) 21:2185-2193
#title Molecular heterogeneity of auto-anti-idiotypic antibodies in
MLR-lpr/lpr mice.

#cross-references MUID:91364791
#accession B49026

#status preliminary; not compared with conceptual translation
#molecule_type nucleic acid
#residues 1-107 #label KOI
#cross-references NCBI:P:60876
#experimental_source MLR-lpr/lpr

#note #sequence extracted from NCBI backbone

REFERENCE PL0220
#authors Puccetti, A.; Koizumi, T.; Migliorini, P.; Andre-Schwartz,
J.; Barrett, K.J.; Schwartz, R.S.
#journal J. Exp. Med. (1990) 171:1919-1930
#title An immunoglobulin light chain from a lupus-prone mouse
induces autoantibodies in normal mice.

#cross-references MUID:90278348
#accession PL0220

#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-107 #label PUC

#experimental_source strain lupus-prone MRL-lpr/lpr mouse
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin

FEATURE 24-34
20-56
89-97
SUMMARY #length 107 #molecular-weight 11859 #checksum 8401
#region complementarity-determining 1\
#region complementarity-determining 2\
#region complementarity-determining 3

Query Match 95.7%; Score 67; DB 7; Length 107;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 6

ENTRY A28044 #type complete
TITLE Ig kappa chain V region (22B5) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-May-1989 #sequence_revision 19-May-1989 #text_change
16-Aug-1996

ACCESSIONS A28044
REFERENCE A94179

#authors Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6244-6248
#title Identity of the V-kappa-10-Ars-A gene segments of the A/J and
BALB/c strains.

#cross-references MUID:87317629
#accession A28044

#molecule_type mRNA

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##residues 1-107 ##label MEE
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 107 #molecular-weight 11832 #checksum 7241

Query Match 95.7%; Score 67; DB 7; Length 107;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 7
ENTRY D48677 #type fragment
TITLE Ig light chain V-J region (24) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-May-1994 #sequence_revision 19-May-1994 #text_change
16-Aug-1996
ACCESSIONS D48677
REFERENCE A48677
#authors Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb,
P.; Brown, A.; Hasemann, C.A.; Capra, J.D.; Meek, K.
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9508-9512
#title Molecular characterization of monoclonal CRI-A-positive
anti-arsenate antibodies derived from idiotypic-negative
mice bearing a light chain polymorphism.
#accession D48677
#status preliminary; not compared with conceptual translation
#molecule_type mRNA
##residues 1-107 ##label TAS
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
SUMMARY #length 107 #checksum 7155

Query Match 95.7%; Score 67; DB 7; Length 107;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 8
ENTRY S69901 #type complete
TITLE Ig kappa light chain (clone KL2.21) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
09-May-1997
ACCESSIONS S69901
REFERENCE S69900
#authors Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
#journal Immunology (1992) 75:116-121
#title B-cell proliferation initiated by Ia cross-linking and
sustained by interleukins leads to class switching but not
somatic mutation in vitro.
#accession S69901
#status preliminary; translation not shown
#molecule_type DNA
##residues 1-107 ##label WYS
##cross-references EMBL:X55042
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 107 #molecular-weight 11857 #checksum 7740

Query Match 95.7%; Score 67; DB 7; Length 107;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
QY 1 RASQDISSYLN 11

##residues 1-107 ##label MEE
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 107 #molecular-weight 11832 #checksum 7241

Query Match 95.7%; Score 67; DB 7; Length 107;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 9
ENTRY S38862 #type complete
TITLE Ig kappa chain V region - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
16-Aug-1996
ACCESSIONS S38862
REFERENCE S37200
#authors Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.;
Kreuzaler, F.
#submission submitted to the EMBL Data Library, August 1993
#description Production and cloning of TMV-specific monoclonal antibodies.
#accession S38862
#status preliminary
#molecule_type mRNA
##residues 1-108 ##label FIS
##cross-references EMBL:X75854
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 108 #molecular-weight 11865 #checksum 1422

Query Match 95.7%; Score 67; DB 7; Length 108;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 10
ENTRY S69903 #type complete
TITLE Ig kappa light chain (clone KL2.29) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
09-May-1997
ACCESSIONS S69903
REFERENCE S69900
#authors Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
#journal Immunology (1992) 75:116-121
#title B-cell proliferation initiated by Ia cross-linking and
sustained by interleukins leads to class switching but not
somatic mutation in vitro.
#accession S69903
#status preliminary; translation not shown
#molecule_type DNA
##residues 1-108 ##label WYS
##cross-references EMBL:X55044
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 108 #molecular-weight 11931 #checksum 1846

Query Match 95.7%; Score 67; DB 7; Length 108;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 11
ENTRY S69902 #type complete
TITLE Ig kappa light chain (clone KL2.28) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
09-May-1997
ACCESSIONS S69902
REFERENCE S69900
#authors Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
#journal Immunology (1992) 75:116-121
#title B-cell proliferation initiated by Ia cross-linking and
```

sustained by interleukins leads to class switching but not somatic mutation in vitro.

#accession S69902
#status preliminary; translation not shown
#residues 1-108 #label WYS

#molecule_type DNA

#cross-references EMBL:X55043
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 108 #molecular-weight 11695 #checksum 1228

Query Match 95.7%; Score 67; DB 7; Length 108;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
Qy 1 RASQDISSYLN 11

RESULT 12
ENTRY S69900 #type complete
TITLE Ig kappa light chain (clone KL2.18) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-May-1997
ACCESSIONS S69900
REFERENCE Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
#authors Immunology (1992) 75:116-121
#journal B-cell proliferation initiated by Ia cross-linking and
#title sustained by interleukins leads to class switching but not somatic mutation in vitro.

#accession S69900
#status preliminary; translation not shown
#molecule_type DNA
#residues 1-108 #label WYS

#cross-references EMBL:X55041
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 108 #molecular-weight 11954 #checksum 1768

Query Match 95.7%; Score 67; DB 7; Length 108;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
Qy 1 RASQDISSYLN 11

RESULT 13
ENTRY KVMSAR #type complete
TITLE Ig kappa chain V regions (anti-arsonate hybridoma proteins) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 16-Aug-1996
ACCESSIONS A01927
REFERENCE Siegelman, M.; Capra, J.D.
#authors Proc. Natl. Acad. Sci. U.S.A. (1981) 78:7679-7683
#journal Complete amino acid sequence of light chain variable regions
#title derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.

#cross-references MUID:82150934
#accession A01927

#molecule_type protein
#residues 1-108 #label STE
#experimental_source strain A/J
#note hp 93C7 differs in having 93-Wet; HP 123E6 differs in having 7-Ser, 92-Tyr, and 93-Met; HP 124E1 differs in having 30-Asn, 92-Lys, and 93-Thr; and HP 91A3 differs in having 8-Pro, 30-Asn, 37-Arg, 84-Ser, and 93-Ala

COMMENT The sequence shown is HP R16.7.
COMPLEX An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer

FEATURE #disulfide_bonds #status predicted
23-88

SUMMARY #length 108 #molecular-weight 11910 #checksum 1537

Query Match 95.7%; Score 67; DB 2; Length 108;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
Qy 1 RASQDISSYLN 11

RESULT 14
ENTRY C26405 #type complete
TITLE Ig kappa chain V region (3D10) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Aug-1996

ACCESSIONS C26405
REFERENCE Smith, J.A.; Margolies, M.N.
#authors Biochemistry (1987) 26:604-612
#journal Complete amino acid sequences of the heavy and light chain
#title variable regions from two A/J mouse antigen nonbinding monoclonal antibodies bearing the predominant p-azophenyl

arsonate idiotype.
#cross-references MUID:87157677
#accession C26405

#molecule_type protein
#residues 1-108 #label SMI
#experimental_source strain A/J

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 108 #molecular-weight 11944 #checksum 1684

Query Match 95.7%; Score 67; DB 7; Length 108;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
|||||:||||
Qy 1 RASQDISSYLN 11

RESULT 15
ENTRY PL0282 #type fragment
TITLE Ig light chain V region (45-49, anti p-azophenylarsonate) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

ACCESSIONS PL0282
REFERENCE Wysocki, L.J.; Gifter, M.L.; Margolies, M.N.

#authors J. Exp. Med. (1990) 172:315-323
#journal Parallel evolution of antibody variable regions by somatic processes: Consecutive shared somatic alterations in VH genes expressed by independently generated hybridomas apparently acquired by point mutation and selection rather than by gene conversion.

#accession PL0282
#molecule_type mRNA
#residues 1-108 #label WYS

```
##experimental_source A/J mice
CLASSIFICATION #superfamily immunoglobulin v region; immunoglobulin homology
KEYWORDS immunoglobulin
SUMMARY #length 108 #checksum 960

Query Match 95.7%; Score 67; DB 7; Length 108;
Best Local Similarity 90.9%; Pred. No. 5.82e-03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisnyln 34
| | | | | | | | | |
QY 1 RASQDISSYLN 11
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Search completed: Tue Mar 3 11:19:18 1998
Job time : 11 secs.
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WQSEFH
***** (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Mar 3 11:18:38 1998; MasPar time 2.03 Seconds
Tabular output not generated. 114.979 Million cell updates/sec

Title: >US-08-137-117D-117
Description: (1-11) from US08137117D.pep
Perfect Score: 70
Sequence: 1 RASQDISSYLN 11

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 24.439; Variance 27.038; scale 0.904

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	67	95.7	108	5	KV5K_MOUSE	IG KAPPA CHAIN V-V RE	2.56e-04
2	67	95.7	108	5	KV5N_MOUSE	IG KAPPA CHAIN V-V RE	2.56e-04
3	67	95.7	108	5	KV5L_MOUSE	IG KAPPA CHAIN V-V RE	2.56e-04
4	64	91.4	108	5	KV5Q_MOUSE	IG KAPPA CHAIN V-V RE	1.50e-03
5	64	91.4	108	5	KV5N_MOUSE	IG KAPPA CHAIN V-V RE	1.50e-03
6	63	90.0	108	5	KVIN_HUMAN	IG KAPPA CHAIN V-I RE	2.68e-03
7	61	87.1	117	5	KV5H_MOUSE	IG KAPPA CHAIN PRECUR	8.44e-03
8	61	87.1	129	5	KVIN_HUMAN	IG KAPPA CHAIN PRECUR	8.44e-03
9	60	85.7	108	5	KV1H_HUMAN	IG KAPPA CHAIN V-I RE	1.48e-02
10	58	82.9	108	5	KV1B_HUMAN	IG KAPPA CHAIN V-I RE	4.52e-02
11	58	82.9	108	5	KV1Y_HUMAN	IG KAPPA CHAIN V-I RE	4.52e-02
12	58	82.9	108	5	KV5U_MOUSE	IG KAPPA CHAIN PRECUR	4.52e-02
13	58	82.9	115	5	KV5F_MOUSE	IG KAPPA CHAIN PRECUR	4.52e-02
14	57	81.4	115	5	KV3I_HUMAN	IG KAPPA CHAIN PRECUR	7.81e-02
15	57	81.4	128	5	KV5E_MOUSE	IG KAPPA CHAIN PRECUR	7.81e-02
16	54	77.1	108	5	KV5P_MOUSE	IG KAPPA CHAIN V-V RE	3.90e-01
17	53	75.7	108	5	KV1A_HUMAN	IG KAPPA CHAIN V-I RE	6.57e-01
18	52	74.3	108	5	KV1M_HUMAN	IG KAPPA CHAIN V-I RE	1.10e+00
19	51	72.9	108	5	KV1E_HUMAN	IG KAPPA CHAIN V-I RE	1.83e+00
20	51	72.9	130	5	KV5G_MOUSE	IG KAPPA CHAIN PRECUR	1.83e+00
21	51	72.9	382	2	CARA_ECOLI	CARBAMOYL-PHOSPHATE S	1.83e+00
22	51	72.9	382	2	CARA_SALTY	CARBAMOYL-PHOSPHATE S	1.83e+00

23	50	71.4	107	5	KVID_HUMAN	IG KAPPA CHAIN V-I RE	3.02e+00
24	50	71.4	108	5	KV5D_MOUSE	IG KAPPA CHAIN V-V RE	3.02e+00
25	50	71.4	108	5	KV1P_HUMAN	IG KAPPA CHAIN V-I RE	3.02e+00
26	50	71.4	108	5	KV07_RABIT	IG KAPPA CHAIN V REGI	3.02e+00
27	50	71.4	108	5	KV10_HUMAN	IG KAPPA CHAIN V-I RE	3.02e+00
28	50	71.4	117	5	KV10_RABIT	IG KAPPA CHAIN V REGI	3.02e+00
29	50	71.4	1342	3	ERB3_HUMAN	ERBB-3 RECEPTOR PROTE	3.02e+00
30	49	70.0	108	5	KV5J_MOUSE	IG KAPPA CHAIN V-V RE	4.95e+00
31	48	68.6	133	8	PSSR_ECOLI	POSSIBLE REGULATORY P	8.04e+00
32	48	68.6	199	7	PRL_BALBO	PROLACTIN (PRL).	8.04e+00
33	48	68.6	199	7	PRL_LOXAF	PROLACTIN (PRL).	8.04e+00
34	48	68.6	229	7	PRL_FELCA	PROLACTIN PRECURSOR	8.04e+00
35	48	68.6	312	6	NIFU_AZOVI	NIFU PROTEIN.	8.04e+00
36	47	67.1	108	5	KV1S_HUMAN	IG KAPPA CHAIN V-I RE	1.30e+01
37	47	67.1	117	5	KV1J_HUMAN	IG KAPPA CHAIN PRECUR	1.30e+01
38	47	67.1	129	5	KV1X_HUMAN	IG KAPPA CHAIN PRECUR	1.30e+01
39	47	67.1	199	11	YAGU_RABIN	HYPOTHETICAL LIPOPROT	1.30e+01
40	47	67.1	235	11	YI01_YEAST	HYPOTHETICAL 27.1 KD	1.30e+01
41	47	67.1	274	9	T2E1_HERAU	TYPE II RESTRICTION E	1.30e+01
42	47	67.1	943	5	IROA_NEIME	IRON-REGULATED OUTER	1.30e+01
43	46	65.7	451	7	PHOQ_SALTY	VIRULENCE SENSOR PROT	2.07e+01
44	46	65.7	1132	10	VHSI_LAMB	HOST SPECIFICITY PROT	2.07e+01
45	46	65.7	1507	11	YY06_HUMAN	HYPOTHETICAL MYELOID	2.07e+01

ALIGNMENTS

RESULT 1
ID KV5K_MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-V REGION (HP R16.7).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RC STRAIN-A/J;
RX MEDLINE; 82150934.
RA SIEGELMAN M., CAPRA J.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KWSAR.
DR HSP: P01607; 1FAI.
KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11910 MW; 64A62905 CRC32;
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
FRAMEWORK 4.
BY SIMILARITY.

Query Match 95.7%; Score 67; DB 5; Length 108;
Best Local Similarity 90.9%; Pred. No. 2.56e-04;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisynln 34
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 2
ID KV5M_MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN V-V REGION (HP 123E6).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE; 82150934.
 RA SIEGELMAN M., CAPRA J.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
 CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR; A01927; KVMAR.
 DR HSP; P01607; IFAI.
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11989 MW; 23B8BB67 CRC32;

Query Match 95.7%; Score 67; DB 5; Length 108;

Best Local Similarity 90.9%; Pred. No. 2.56e-04; Length 108;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisynln 34
 |||||:||||
 QY 1 RASQDISSYLN 11

RESULT 3
 ID KV5L_MOUSE STANDARD; PRT; 108 AA.
 AC P01645;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-V REGION (HP 93G7).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE; 82150934.
 RA SIEGELMAN M., CAPRA J.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
 CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR; A01927; KVMAR.
 DR HSP; P01607; IFAI.
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11954 MW; A203E130 CRC32;

Query Match 95.7%; Score 67; DB 5; Length 108;
 Best Local Similarity 90.9%; Pred. No. 2.56e-04;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisynln 34
 |||||:||||
 QY 1 RASQDISSYLN 11

RESULT 4
 ID KV5O_MOUSE STANDARD; PRT; 108 AA.
 AC P01648;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-V REGION (HP 91A3).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE; 82150934.
 RA SIEGELMAN M., CAPRA J.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
 CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR; A01927; KVMAR.
 DR HSP; P01607; IFAI.
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11961 MW; 5B067780 CRC32;

Query Match 91.4%; Score 64; DB 5; Length 108;

Best Local Similarity 81.8%; Pred. No. 1.50e-03; Length 108;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisynln 34
 |||||:||||
 QY 1 RASQDISSYLN 11

RESULT 5
 ID KV5N_MOUSE STANDARD; PRT; 108 AA.
 AC P01647;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-V REGION (HP 124E1).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE; 82150934.
 RA SIEGELMAN M., CAPRA J.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
 CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR; A01927; KVMAR.
 DR HSP; P01607; IFAI.
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11965 MW; 84754175 CRC32;

Query Match 91.4%; Score 64; DB 5; Length 108;
 Best Local Similarity 81.8%; Pred. No. 1.50e-03; Length 108;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdisynln 34
 |||||:||||
 QY 1 RASQDISSYLN 11

Best Local Similarity 81.8%; Pred. No. 1.50e-03;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 24 rasqdinayln 34
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 6
ID KVIN_HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (OU).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RA KOHLER H., SHIMIZU A., PAUL C., PUTNAM F.W.;
RL SCIENCE 169:56-59(1970).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR; A01872; K1HUOU.
DR HSP; P01607; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 4B089785 CRC32;

Query Match 90.0%; Score 63; DB 5; Length 108;
Best Local Similarity 72.7%; Pred. No. 2.68e-03;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 24 rasztissylb 34
|||:|||||
QY 1 RASQDISSYLN 11

RESULT 7
ID KV5H_MOUSE STANDARD; PRT; 117 AA.
AC P01641;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 173B).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81064681.
RA MAX E.E., SEIDMAN J.G., MILLER H., LEDER P.;
RL CELL 21:793-799(1980).
DR EMBL; K00860; G197444; -.
DR PIR; A01924; KVM33B.
DR HSP; P01607; 1FGV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 22
FT CHAIN 23 117
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
IG KAPPA CHAIN V-V REGION (MOPC 173B).
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
FRAMEWORK 4.
BY SIMILARITY.

FT DOMAIN 79 110
FT DOMAIN 111 >117
FT DISULFID 45 110
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12954 MW; 38F2B08C CRC32;

Query Match 87.1%; Score 61; DB 5; Length 117;
Best Local Similarity 81.8%; Pred. No. 8.44e-03;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 46 rasqdihsyln 56
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 8
ID KVIN_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-I REGION (WALKER).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85014148.
RA KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 12:6995-7006(1984).
DR EMBL; X00965; G296684; ALT_TERM.
DR PIR; A01883; K1HUWK.
DR HSP; P01607; 2FGW.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 22
FT CHAIN 23 129
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 110
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; 99925172 CRC32;

Query Match 87.1%; Score 61; DB 5; Length 129;
Best Local Similarity 81.8%; Pred. No. 8.44e-03;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 46 rasqsisyln 56
|||||:||||
QY 1 RASQDISSYLN 11

RESULT 9
ID KVIN_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (HAU).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 71032830.
RA WATANABE S., HILSCHMANN N.;
RL HOPPE-SEYLER S. Z. PHYSIOL. CHEM. 351:1291-1295(1970).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- THIS IS A BENICE-JONES PROTEIN.

DR PIR: A01868; K1HUHU.
 DR HSP: P01607; 1FVC.
 KW IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 FRAMEWORK 2.
 FT DOMAIN 35 49 FRAMEWORK 3.
 FT DOMAIN 50 56 FRAMEWORK 4.
 FT DOMAIN 57 88 FRAMEWORK 5.
 FT DOMAIN 89 97 FRAMEWORK 6.
 FT DOMAIN 98 107 FRAMEWORK 7.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; C8A2EE86 CRC32;
 Query Match 85.7%; Score 60; DB 5; Length 108;
 Best Local Similarity 81.8%; Pred. No. 1.48e-02;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 24 rasqdisyn 34
 QY 1 RASQDISSYN 11
 RESULT 10
 ID KVIB_HUMAN STANDARD; PRT; 108 AA.
 AC P01594;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (AU).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX SCHIEHL H., HILSCHMANN N.;
 RX HOPE-SEYLER S. Z. PHYSIOL. CHEM. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE; 77022433.
 RA FEHLHAMMER H., SCHIFFER M., EPP O., COLMAN P.M., LATTMAN E.E.,
 RA SCHWAGER P., STEIGMANN W., SCHRAMM H.J.;
 RL BIOPHYS. STRUCT. MECH. 1:139-146(1975).
 CC -1- THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR
 CC REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF
 CC THE KAPPA CHAIN REL.
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- THIS IS A BENGE-JONES PROTEIN.
 DR PIR: A01862; K1HUHU.
 DR HSP: P01607; 1IGM.
 KW IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 FRAMEWORK 4.
 FT DOMAIN 98 107 FRAMEWORK 5.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; B455AF00 CRC32;
 Query Match 82.9%; Score 58; DB 5; Length 108;
 Best Local Similarity 81.8%; Pred. No. 4.52e-02;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 24 rasqdisyn 34
 QY 1 RASQDISSYN 11
 RESULT 11

ID KVIV_HUMAN STANDARD; PRT; 108 AA.
 AC P80362;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-I REGION (WAT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE; 95086080.
 RA HUANG D.-B., CHANG C.-H., AINSWORTH C., BRUENGER A.T., EULITZ M.,
 RA SOLOMON A., STEVENS F.J., SCHIFFER M.;
 RL BIOCHEMISTRY 33:14848-14857(1994).
 RN [2]
 RP SEQUENCE OF 1-35.
 RX MEDLINE; 81267384.
 RA STEVENS F.J., WESTHOLM F.A., PANAGIOTOPOULOS N., SCHIFFER M.,
 RA POPP R.A., SOLOMON A.;
 RL J. MOL. BIOL. 147:185-193(1981).
 CC -1- THIS IS A BENGE-JONES PROTEIN.
 DR PDB; 1WTL; 01-NOV-94.
 KW IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN; 3D-STRUCTURE.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT CONFLICT 30 31 TN -> SD (IN REF. 2).
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; 41A2388C CRC32;
 Query Match 82.9%; Score 58; DB 5; Length 108;
 Best Local Similarity 72.7%; Pred. No. 4.52e-02;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Db 24 rasqdisyn 34
 QY 1 RASQDISSYN 11
 RESULT 12
 ID KV5U_MOUSE STANDARD; PRT; 108 AA.
 AC P04946;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-V REGION (N05-89.4).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 83271467.
 RA KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;
 RL NATURE 304:320-324(1983).
 CC -1- ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
 DR EMBL; K00745; G196455; -.
 DR HSP; P01607; 1PAI.
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108

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SQ SEQUENCE 108 AA; 11866 MW; D396F142 CRC32;
Query Match      82.9%; Score 58; DB 5; Length 108;
Best Local Similarity 90.0%; Pred. No. 4.52e-02;
Matches      9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db      25 asqdisnyln 34
        |||||:||||
QY      2 ASQDISSYLN 11

RESULT 13
ID KVSF_MOUSE STANDARD; PRT; 115 AA.
AC P01638;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-V REGION (L6) (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81220975.
RA PECH M., HOCHTL J., SCHNELL H., ZACHAU H.G.;
RL NATURE 291:668-670(1981).
DR PIR: A01921; KVMSL6.
DR HSP: P01607; I1IF.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION (L6).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12986 MW; 958689AF CRC32;

Query Match      82.9%; Score 58; DB 5; Length 115;
Best Local Similarity 72.7%; Pred. No. 4.52e-02;
Matches      8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db      44 kasqdisnyls 54
        :|||||:||||
QY      1 RASQDISSYLN 11

RESULT 14
ID KV31_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85087932.
RA PECH M., ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 12:9229-9236(1984).
DR EMBL; X01668; -: NOT_ANNOTATED_CDS.
DR PIR: A01900; K3HUVG.
DR HSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION (VG).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
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FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 37E182FC CRC32;

Query Match      81.4%; Score 57; DB 5; Length 115;
Best Local Similarity 80.0%; Pred. No. 7.81e-02;
Matches      8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db      44 rasqsvssyl 53
        ||||:||||
QY      1 RASQDISSYLN 10

RESULT 15
ID KV5E_MOUSE STANDARD; PRT; 128 AA.
AC P01637;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-V REGION (T1).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81052342.
RA ALTENBURGER W., STEINMETZ M., ZACHAU H.G.;
RL NATURE 287:603-607(1980).
DR EMBL; V00772; G762979; -.
DR PIR: A01920; KVMST1.
DR HSP: P01607; I1IF.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION (T1).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 127 FRAMEWORK 4.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14385 MW; 87009E44 CRC32;

Query Match      81.4%; Score 57; DB 5; Length 128;
Best Local Similarity 80.0%; Pred. No. 7.81e-02;
Matches      8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db      44 kasqdisnyl 53
        :|||||:||||
QY      1 RASQDISSYLN 10
```

Search completed: Tue Mar 3 11:18:47 1998
Job time : 9 secs.

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W P E R L H
***** (TW)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 3 14:28:08 1998; Maspar time 8.47 Seconds
Tabular output not generated. 11.473 Million cell updates/sec

Title: >US-08-137-117D-118
Description: (1-7) from US08137117D.pap
Perfect Score: 51
Sequence: 1 YTSRLHS 7

Scoring table:
PAM 150
Gap 15

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 15.572; Variance 37.259; scale 0.418

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	51	100.0	88	9 R47210	Chimeric human/mouse	5.83e+00
2	51	100.0	107	6 R30768	Murine anti-CD3 Mab U	5.83e+00
3	51	100.0	108	20 W00834	Variable light chain	5.83e+00
4	51	100.0	108	20 W04177	Variant variable light	5.83e+00
5	51	100.0	109	17 R52039	Light chain variable	5.83e+00
6	51	100.0	124	9 R47206	Human/murine IL-1 chi	5.83e+00
7	51	100.0	126	5 R29015	pUC-RV1-PM1a.	5.83e+00
8	51	100.0	126	5 R29013	pUC-RVh-PM1a.	5.83e+00
9	51	100.0	127	22 W11815	Mouse anti-human Fas	5.83e+00
10	51	100.0	127	22 W11817	Humanised mouse anti-	5.83e+00
11	51	100.0	127	5 R28670	ppM-K3 protein produc	5.83e+00
12	51	100.0	127	5 R32121	Anti-CD4 antibody MT	5.83e+00
13	51	100.0	128	19 W06215	MAB ME4 light chain v	5.83e+00
14	51	100.0	128	5 R09426	ME4 Light Chain V Reg	5.83e+00
15	51	100.0	129	9 R47207	Human/murine IL-1 chi	5.83e+00
16	51	100.0	131	14 R84553	MAB SCH94.03 light ch	5.83e+00
17	51	100.0	268	8 R44226	Chimeric Ig superami	5.83e+00
18	51	100.0	302	10 R60206	Bispecific CD3-L6Fvlg	5.83e+00
19	46	90.2	127	19 R99003	MAB VIL17B6 light chai	2.76e+01
20	45	90.2	1422	16 R82071	Hepatitis GB virus (H	2.76e+01

21	42	82.4	107	6 R30769	huxCD3v9, humanised m	9.19e+01
22	42	82.4	140	5 R77559	Cyn d allergen Bl.	9.19e+01
23	41	80.4	107	13 R7302	Variable light chain	1.23e+02
24	41	80.4	126	2 R12237	Mouse Mab 1C11 L chai	1.23e+02
25	41	80.4	127	2 R12359	Light (kappa) chain v	1.23e+02
26	41	80.4	273	9 R52865	Anti-Influenza N10 sc	1.23e+02
27	41	80.4	539	21 W20778	H. pylori cytoplasmic	1.23e+02
28	40	78.4	127	7 R39265	Mouse C4G1 Ig light-c	1.65e+02
29	40	78.4	172	17 W00482	Human deoxycytidine k	1.65e+02
30	40	78.4	214	6 R30776	H52L6-158 murine anti	1.65e+02
31	40	78.4	214	19 W00373	Anti-CD18 chimeric an	1.65e+02
32	40	78.4	214	7 R43338	Completely humanised	1.65e+02
33	40	78.4	233	6 R30777	PH52-9.0 humanised mu	1.65e+02
34	40	78.4	706	12 R68743	BCL-6 zinc finger pro	1.65e+02
35	40	78.4	1235	22 W21572	Rat brain serine ecto	1.65e+02
36	40	78.4	1249	22 W21571	Rat brain homologue o	1.65e+02
37	39	76.5	127	5 R39010	p146-k3 protein produ	2.20e+02
38	39	76.5	432	15 R2813	Murine interleukin-11	2.20e+02
39	39	76.5	441	17 R99091	Murine Etl-2 gene pro	2.20e+02
40	39	76.5	928	14 R77399	BHV1 gI glycoprotein.	2.20e+02
41	39	76.5	933	5 R27807	Bovine herpes virus t	2.20e+02
42	39	76.5	933	7 R41343	Bovine herpesvirus ty	2.20e+02
43	38	74.5	745	13 R76110	Human ALD.	2.93e+02
44	38	74.5	794	23 W25637	Human cadherin-12.	2.93e+02
45	38	74.5	842	4 P93712	Sequence of infectiou	2.93e+02

ALIGNMENTS

RESULT 1
ID R47210 standard; Protein; 88 AA.
AC R47210;
DT 09-AUG-1994 (first entry)
DE Chimeric human/mouse antibody L chain mature peptide.
KW Probe; chimeric; recombinant; antibody; human; interleukin-1; IL-1;
KW light; L; chain; constant; region; variable; mouse; anti-human; PCR;
KW graft; CDR; complementarity determining region; heavy; H; detection;
KW inflammatory disease; arteriosclerosis; polymerase chain reaction;
KW diffused intravascular coagulation; leukemia; amplify.
OS Chimeric - Homo sapiens.
OS Chimeric - Mus musculus.
PN W094032627-A.
PD 03-FEB-1994.
PF 08-JUL-1993; J00941.
PR 16-JUL-1992; JP-189248.
PA (SAXA) OHSUKA PHARM CO LTD.
PI Hirai Y, Nishida T, Omoto Y, Owens RJ;
DR WPI; 94-048885/06.
DR N-PSDB; Q56075.
PT Mouse/human chimeric antibody against human interleukin-1 - for
PT treatment of diseases in which production of interleukin-1 is
PT abnormal, and for diagnostic imaging of interleukin-1 production
PT sites in vivo
PS Disclosure; Fig 18; 58pp; Japanese.
CC This sequence represents the mature L chain of a chimeric recombinant
CC antibody against human interleukin-1 (IL-1). The chimeric antibody
CC has a light (L) chain in which the constant region is that of a human
CC antibody and the variable region is from a mouse anti-human IL-1
CC antibody or is a mouse-human graft containing the CDR regions of mouse
CC anti-human IL-1 antibody, and a heavy (H) chain in which the constant
CC region is that of a human antibody and the variable region is from a
CC mouse anti-human IL-1 antibody or is a mouse-human graft containing
CC the CDR regions of mouse anti-human IL-1 antibody. The chimeric
CC antibody is used to treat diseases in which abnormal amounts of IL-1
CC are produced, eg. inflammatory disease, arteriosclerosis, diffused
CC intravascular coagulation or leukemia. It can also be labelled and
CC used for diagnostic imaging of IL-1 producing sites in vivo.
SQ Sequence 88 AA;

Query Match 100.0%; Score 51; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 5.83e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 34 ytsrlhs 40
 1 YTSRLHS 7
 Best Local Similarity 100.0%; Pred. No. 5.83e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 ID R30768 standard; protein; 107 AA.
 AC R30768;
 DT 12-MAY-1993 (first entry)
 DE Murine anti-CD3 MAB UCHT1 light chain variable domain.
 KW Humanisation; rapid; monoclonal antibody; muxCD3.
 OS Mus musculus.
 PN WO9222653-A.
 PD 23-DEC-1992.
 PF 15-JUN-1992; U05126.
 PR 14-JUN-1991; US-715272.
 PA (GETH) GENENTECH INC.
 PI Carter PJ, Presta LG.
 DR WPI; 93-018139/02.
 PT Humanisation of antibodies - by molecular modelling of the variable domains and alteration by gene conversion mutagenesis.
 PS Disclosure; Fig 5; 126pp; English.
 CC The sequence is that of the light chain variable domain of murine anti-CD3 monoclonal antibody UCHT1 (muxCD3, Shalaby 1992).
 SQ Sequence 107 AA;

Query Match 100.0%; Score 51; DB 6; Length 107;
 Best Local Similarity 100.0%; Pred. No. 5.83e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 ytsrlhs 56
 1 YTSRLHS 7

RESULT 3
 ID W00834 standard; Protein; 108 AA.

AC W00834;
 DT 20-MAY-1997 (first entry)
 DE Variable light chain of anti-human Fas ligand antibody NOK-1.
 KW Variable region; light chain; human; Fas ligand; monoclonal;
 KW antibody; NOK-1; hybridoma; inhibition; apoptosis; assay;
 KW diagnosis; disease; hepatitis; infectious mononucleosis;
 KW systemic lupus erythematosus.
 OS Mus musculus.
 PN WO9629350-A1.
 PD 26-SEP-1996.
 PF 21-MAR-1996; J00734.
 PR 20-MAR-1995; JP-087420.
 PR 27-OCT-1995; JP-303492.
 PA (SUME) SUMITOMO ELECTRIC IND CO.
 PI Kayagaki N, Nakata M, Okumura K, Yagita H;
 DR WPI; 96-443140/44.

DR N-PSDB; T39560.
 DT Monoclonal antibody specifically recognising the Fas ligand - useful for the detection of Fas ligands either on cell surface or in solution
 PS Claim 41; Pages 93-94; 133pp; Japanese.
 CC The present sequence is the light chain variable region of the anti-human Fas ligand monoclonal antibody (MAB) NOK-1. NOK-1 is produced by the hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice with transformed human Fas ligand expressing COS cells, and fusing spleen cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580) cells. The MAB recognises the human Fas ligand on the cell surface or in solution, and can be used to inhibit the apoptosis inducing cell surface Fas ligand/Fas reaction. The MAB can also be used for a Fas ligand assay in biological samples (e.g. human blood), especially for disease diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus erythematosus.
 SQ Sequence 108 AA;

Query Match 100.0%; Score 51; DB 20; Length 108;

Best Local Similarity 100.0%; Pred. No. 5.83e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 ytsrlhs 56
 1 YTSRLHS 7

RESULT 4
 ID W04177 standard; Protein; 108 AA.

AC W04177;
 DT 19-MAY-1997 (first entry)
 DE Variant variable light chain of Fas ligand antibody NOK-1.
 KW Variable region; light chain; human; Fas ligand; monoclonal;
 KW antibody; NOK-1; hybridoma; inhibition; apoptosis; assay;
 KW diagnosis; disease; hepatitis; infectious mononucleosis;
 KW systemic lupus erythematosus; variant.
 OS Mus musculus.
 PN WO9629350-A1.
 PD 26-SEP-1996.
 PF 21-MAR-1996; J00734.
 PR 20-MAR-1995; JP-087420.
 PR 27-OCT-1995; JP-303492.
 PA (SUME) SUMITOMO ELECTRIC IND CO.
 PI Kayagaki N, Nakata M, Okumura K, Yagita H;
 DR WPI; 96-443140/44.

DR N-PSDB; T39550.
 DT Monoclonal antibody specifically recognising the Fas ligand - useful for the detection of Fas ligands either on cell surface or in solution
 PS Claim 20; Pages 80-81; 133pp; Japanese.
 CC The present sequence is a variant light chain variable region of the anti-human Fas ligand monoclonal antibody (MAB) NOK-1. NOK-1 is produced by the hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice with transformed human Fas ligand expressing COS cells, and fusing spleen cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580) cells. The MAB recognises the human Fas ligand on the cell surface or in solution, and can be used to inhibit the apoptosis inducing cell surface Fas ligand/Fas reaction. The MAB can also be used for a Fas ligand assay in biological samples (e.g. human blood), especially for disease diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus erythematosus.
 SQ Sequence 108 AA;

Query Match 100.0%; Score 51; DB 20; Length 108;

Best Local Similarity 100.0%; Pred. No. 5.83e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 ytsrlhs 56
 1 YTSRLHS 7

RESULT 5
 ID R52039 standard; Protein; 109 AA.

AC R52039;
 DT 27-SEP-1996 (first entry)
 DE Light chain variable region of murine antibody lfl9.
 KW antibody; humanised; murine; heavy chain; light; variable;
 KW framework region; complementarity determining region; reshaping;
 KW modelling; surface residue; modify.
 OS Mus sp.

FT Key Location/Qualifiers
 FT Region 1..23
 FT /label= framework_region_1
 FT /note= "FR 1"
 FT Region 24..34
 FT /label= complementarity_determining_region_1
 FT /note= "CDR 1"
 FT Region 35..49
 FT /label= FR_2
 FT Region 50..56

FT /label= CDR_2 57..88
FT Region /label= FR_3
FT Region 89..97
FT /label= CDR_3 98..109
FT Region /label= FR_4
FT /label= FR_4
PN EP-592106-A1.
PD 13-APR-1994. 307051.
PF 07-SEP-1993; 307051.
PR 09-SEP-1992; US-942245.
PA (PEDE/) PEDERSEN J T.
PA (IMMU-) IMMUNOGEN INC.
PI Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
DR WPI: 94-120230/15.

PT Method of resurfacing of rodent antibodies to produce humanised
PT antibody forms - for producing non-human antibodies with improved
PT therapeutic efficiency by presenting human surface on V-region
PS Example 1; Fig 3A; 230pp; English.
CC The present sequence is that of the light chain variable (LC VR) region
CC of murine antibody 1f19. This sequence was aligned with 11 other known
CC antibody LC VRs and a set of framework positions of surface exposed amino
CC acid residues was determined. This information can be used in a method to
CC determine how to modify a rodent antibody or fragment by resurfacing in
CC order to produce a humanised rodent antibody. Residues (determined from
CC alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86,
CC 87, 111, 115, 116 and 117 are accessible residues. None of the entire
CC combinations of surface residues in the murine sequences were found in
CC the human sequences and vice versa. However the residues in individual
CC positions appear to be conserved.
SQ Sequence 109 AA;

Query Match 100.0%; Score 51; DB 17; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.83e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 ytsrlhs 56
QY 1 YTSRLHS 7
|||||

RESULT 6

ID R47206 standard; Protein; 124 AA.
AC R47206;
DT 09-AUG-1994 (first entry)
DE Human/murine IL-1 chimeric antibody CH.
KW Probe; chimeric; recombinant; antibody; human; interleukin-1; IL-1;
KW light; L; chain; constant; region; variable; mouse; anti-human;
KW graft; CDR; complementarity determining region; heavy; H;
KW inflammatory disease; arteriosclerosis; detection;
KW diffused intravascular coagulation; leukemia.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..17
FT /note= "Signal peptide"
FT Protein 18..124
FT /note= "Mature protein"
FN WO9402627-A.
PD 03-FEB-1994.
PF 08-JUL-1993; J00941.
PR 16-JUL-1992; JP-189248.
PA (SARA) OTSUKA PHARM CO LTD.
PI Hirai Y, Nishida T, Omoto Y, Owens RJ;
DR WPI: 94-048885/06.
DR N-PSDB; Q36067.
PT Mouse/human chimeric antibody against human interleukin-1 - for
PT treatment of diseases in which production of interleukin-1 is
PT abnormal, and for diagnostic imaging of interleukin-1 production
PT sites in vivo
PS Claim 1; Page 31-32; 58pp; Japanese.
CC The sequences given in R47205-08 represent the light and heavy chain,
CC variable and constant regions of a chimeric recombinant antibody
CC against human interleukin-1 (IL-1). The antibody has a light (L)

CC chain in which the constant region is that of a human antibody and
CC the variable region is from a mouse anti-human IL-1 antibody or is a
CC mouse-human graft containing the CDR regions of mouse anti-human IL-1
CC antibody, and a heavy (H) chain in which the constant region is that
CC of a human antibody and the variable region is from a mouse anti-human
CC IL-1 antibody or is a mouse-human graft containing the CDR regions of
CC mouse anti-human IL-1 antibody. The chimeric antibody is used to
CC treat diseases in which abnormal amounts of IL-1 are produced, eg.
CC inflammatory disease, arteriosclerosis, diffused intravascular
CC coagulation or leukemia. It can also be labelled and used for
CC diagnostic imaging of IL-1 producing sites in vivo.
SQ Sequence 124 AA;

Query Match 100.0%; Score 51; DB 9; Length 124;
Best Local Similarity 100.0%; Pred. No. 5.83e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 67 ytsrlhs 73
QY 1 YTSRLHS 7
|||||

RESULT 7

ID R29015 standard; Protein; 126 AA.
AC R29015;
DT 30-MAR-1993 (first entry)
DE pUC-RV1-PM1a.
KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;
KW complementarity determining region; mouse; monoclonal; hybridoma;
KW plasmid; polymerase chain reaction; amplify.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Leader peptide"
FT Region 20..42
FT /label= FR1 43..53
FT Region /label= CDR1 54..68
FT Region /label= FR2 69..75
FT Region /label= CDR2 76..107
FT Region /label= FR3 108..116
FT Region /label= CDR3 117..126
FT /label= FR4
FN WO9219759-A.
PD 12-NOV-1992. J00544.
PR 24-APR-1992; JP-095476.
PR 25-APR-1991; JP-032084.
PR 19-FEB-1992; JP-032084.
PA (CHUS) CHUGAI SEIYAKU KK.
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WPI: 92-398882/48.
DR N-PSDB; Q31366.

PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PS Disclosure; Page 144-5; 207pp; Japanese.
CC The sequences given in R29012-15 are portions of monoclonal antibodies
CC which were encoded by plasmids derived from mouse hybridomas. The DNA
CC encoding complementarity determining regions (CDR's) was isolated by
CC polymerase chain reaction. These antibodies recognise human
CC interleukin-6 receptor (IL-6R). The mouse hybridoma cells were
CC transformed with the plasmids encoding these genes which caused the
CC secretion of these antibodies from the hybridoma cells.
SQ Sequence 126 AA;

Query Match 100.0%; Score 51; DB 5; Length 126;
Best Local Similarity 100.0%; Pred. No. 5.83e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 69 ytsrlhs 75
 QY 1 YTSRLHS 7

RESULT 8
 ID R29013 standard; Protein; 126 AA.
 AC R29013;
 DT 30-MAR-1993 (first entry)
 DE pUC-RVh-PM1a.
 KW Human; antibody; interleukin-6; receptor; IL-6R; CDR: PCR;
 KW complementarity determining region; mouse; monoclonal; hybridoma;
 KW plasmid; polymerase chain reaction; amplify.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "Leader peptide"
 FT Region 20..42
 FT /label= FR1
 FT Region 43..53
 FT /label= CDR1
 FT Region 54..68
 FT /label= FR2
 FT Region 69..75
 FT /label= CDR2
 FT Region 76..107
 FT /label= FR3
 FT Region 108..116
 FT /label= CDR3
 FT Region 117..126
 FT /label= FR4
 PN WO9219759-A.
 PD 12-NOV-1992.
 PF 24-APR-1992; J00544.
 PR 25-APR-1991; JP-095476.
 PR 19-FEB-1992; JP-032084.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
 DR WPI; 92-398882/48.
 DR N-PSDB; Q31361.
 PT Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 PS Disclosure; Page 140-1; 207pp; Japanese.
 CC The sequences given in R29012-15 are portions of monoclonal antibodies
 CC which were encoded by plasmids derived from mouse hybridomas. The DNA
 CC encoding complementarity determining regions (CDR's) was isolated by
 CC polymerase chain reaction. These antibodies recognise human
 CC interleukin-6 receptor (IL-6R). The mouse hybridoma cells were
 CC transformed with the plasmids encoding these genes which caused the
 CC secretion of these antibodies from the hybridoma cells.
 SQ Sequence 126 AA;

Query Match 100.0%; Score 51; DB 5; Length 126;
 Best Local Similarity 100.0%; Pred. No. 5.83e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 69 ytsrlhs 75
 QY 1 YTSRLHS 7

RESULT 9
 ID W11815 standard; Protein; 127 AA.
 AC W11815;
 DT 20-OCT-1997 (first entry)
 DE Mouse anti-human Fas ligand antibody F919 light chain.
 KW Human; Fas ligand; antigen; neutral; antibody; apoptosis; HIV;
 KW induction; assay; enzyme linked immunosorbent assay; diagnosis;
 KW disease; hepatitis B; hepatitis C; human immunodeficiency virus;
 KW graft versus host disease; ulcerative colitis; sequelae;
 KW myocardial infarction; mouse; murine; monoclonal; treatment;

KW complementarity determining region; CDR.
 OS Mus spp.
 FH Key Location/Qualifiers
 FT Region 44..54
 FT /label= CDR_1
 FT Region 70..76
 FT /label= CDR_2
 FT Region 109..117
 FT /label= CDR_3
 PN WO9702290-A1.
 PD 23-JAN-1997.
 PF 01-JUL-1996; J01820.
 PR 17-MAY-1996; US-649100.
 PR 30-JUN-1995; JP-188480.
 PA (MOCH) MOCHIDA PHARM CO LTD.
 PA (OSAB-) OSAKA BIOSCIENCE INST.
 PI Co MS, Matsusue T, Nagata S, Shirakawa K, Vasquez M;
 DR WPI; 97-108917/10.
 DR N-PSDB; T59500.
 PT Antibody reactive with Fas ligand capable of inducing apoptosis -
 PT used for diagnostic assay of Fas ligand in body fluids and for
 PT treatment of diseases in which Fas ligand/Fas antigen is involved
 PS Claim 5; Fig 10; 164pp; Japanese.
 CC The present sequence is the light chain of the mouse
 CC anti-apoptosis inducing human Fas ligand, monoclonal antibody,
 CC F919. The antibody can be used in a Fas ligand assay, e.g. an
 CC enzyme linked immunosorbent assay, to diagnose diseases in which
 CC the Fas ligand/Fas antigen system is implicated, e.g. hepatitis
 CC B/C, human immunodeficiency virus, graft/host disorders,
 CC ulcerative colitis or sequelae of myocardial infarction. The
 CC antibody may also be used to treat such diseases.
 SQ Sequence 127 AA;

Query Match 100.0%; Score 51; DB 22; Length 127;
 Best Local Similarity 100.0%; Pred. No. 5.83e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 ytsrlhs 76
 QY 1 YTSRLHS 7

RESULT 10
 ID W11817 standard; Protein; 127 AA.
 AC W11817;
 DT 20-OCT-1997 (first entry)
 DE Humanised mouse anti-human Fas ligand antibody F919 light chain.
 KW Human; Fas ligand; antigen; neutral; antibody; apoptosis; HIV;
 KW induction; assay; enzyme linked immunosorbent assay; diagnosis;
 KW disease; hepatitis B; hepatitis C; human immunodeficiency virus;
 KW graft versus host disease; ulcerative colitis; sequelae; chimeric;
 KW myocardial infarction; mouse; murine; monoclonal; treatment.
 OS Chimeric - Mus spp.
 OS Chimeric - Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Region 44..54
 FT /label= CDR_1
 FT Region 70..76
 FT /label= CDR_2
 FT Region 109..117
 FT /label= CDR_3
 PN WO9702290-A1.
 PD 23-JAN-1997.
 PF 01-JUL-1996; J01820.
 PR 17-MAY-1996; US-649100.
 PR 30-JUN-1995; JP-188480.
 PA (MOCH) MOCHIDA PHARM CO LTD.
 PA (OSAB-) OSAKA BIOSCIENCE INST.
 PI Co MS, Matsusue T, Nagata S, Shirakawa K, Vasquez M;
 DR WPI; 97-108917/10.
 DR N-PSDB; T59502.
 PT Antibody reactive with Fas ligand capable of inducing apoptosis -

PT used for diagnostic assay of Fas ligand in body fluids and for
 PT treatment of diseases in which Fas ligand/Fas antigen is involved
 PS Claim 5; Fig 12; 164pp; Japanese.
 CC The present sequence is the light chain of the humanised
 CC mouse anti-apoptosis inducing human Fas ligand, monoclonal
 CC antibody, F919. The antibody can be used in a Fas ligand assay,
 CC e.g. an enzyme linked immunosorbent assay, to diagnose diseases
 CC in which the Fas ligand/Fas antigen system is implicated, e.g.
 CC hepatitis B/C, human immunodeficiency virus, graft/host disorders,
 CC ulcerative colitis or sequelae of myocardial infarction. The
 CC antibody may also be used to treat such diseases.
 SQ Sequence 127 AA;

Query Match 100.0%; Score 51; DB 22; Length 127;

Best Local Similarity 100.0%; Pred. No. 5.83e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 ytsrlhs 76

QY 1 YTSRLHS 7

RESULT 11

ID R28670 standard; Protein; 127 AA.

AC R28670;

DT 30-MAR-1993 (first entry)

DE pPM-k3 protein product.

KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;

KW heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;

KW plasmid; pPM-k3; pPM-hl.

OS Synthetic.

FH Key Location/Qualifiers

FT Peptide 1..20

FT /note= "Signal peptide"

FT Protein 21..127

FT /note= "Mature peptide"

PN W09219759-A.

PD 12-NOV-1992.

PF 24-APR-1992; J00544.

PR 25-APR-1991; JP-095476.

PR 19-FEB-1992; JP-032084.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;

DR WPI; 92-398882/48.

DR N-PSDB; Q30755.

PT Reconstituted human antibody to human interleukin-6 receptor -

PT has low antigenicity and contains mouse V-region complementarity

PT determining regions

PS Disclosure; Page 121-122; 207pp; Japanese.

CC The sequences given in R28670-71 were encoded by plasmids which were

CC used in example to illustrate the production of a human antibody which

CC recognises human interleukin-6 receptor (IL-6R). The antibody

CC comprises light (L) chain and heavy (H) chain variable regions which

CC were derived from a mouse monoclonal antibody produced from the

CC hybridoma PM1 which contained the plasmids pPM-k3 and pPM-hl.

SQ Sequence 127 AA;

Query Match

Best Local Similarity 100.0%; Score 51; DB 5; Length 127;

Pred. No. 5.83e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 ytsrlhs 76

QY 1 YTSRLHS 7

RESULT 12

ID R32121 standard; Protein; 127 AA.

AC R32121;

DT 02-JUN-1993 (first entry)

DE Anti-CD4 antibody MT 15.1 light chain variable region.

KW immunosuppression; tissue transplantation; graft; L chain; V region;

KW T-helper cell inhibition; transplanted rejection; MAB;

KW interleukin-2 receptor.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= signal 21..115
 FT Region
 FT /label= Variable 116..127
 FT Region
 FT /label= J2
 PN DE4143214-A.
 PD 28-JAN-1993. 143214.
 PF 30-DEC-1991; DE-124759.
 PR 25-JUL-1991; DE-124759.
 PR 30-DEC-1991; DE-143214.
 PI (BOEF) BOEHRINGER MANNHEIM GMBH.
 PI Kaluza B, Rietmueller G, Scheuer W, Weidle U;
 DR WPI; 93-037582/05.
 DR N-PSDB; Q36607.
 PT Synergistic antibody compsn. for use as immunosuppressant -
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
 PT alpha- or anti-IL2R beta antibodies
 PS Claim 5; Page 9; 18pp; German.
 CC This sequence is the light chain variable region of a preferred
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic
 CC composition. MAB MT 15.1 is deposited as clone 15-1/F3/14 (SCACC
 CC 90090705). The anti-CD4 antibody is used with at least one anti-IL2R
 CC alpha or beta antibody. Individually the antibodies are strongly
 CC inhibiting and when used together their immunosuppressive properties
 CC are improved; they synergistically inhibit T-helper cell
 CC proliferation to effectively inhibit transplant rejection at low
 CC doses without significantly reducing the general immune response.
 CC See also Q36608-Q36616.
 SQ Sequence 127 AA;

Query Match 100.0%; Score 51; DB 6; Length 127;

Best Local Similarity 100.0%; Pred. No. 5.83e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 ytsrlhs 76

QY 1 YTSRLHS 7

RESULT 13

ID W06215 standard; Protein; 128 AA.

AC W06215;

DT 13-FEB-1997 (first entry)

DE MAB ME4 light chain variable region.

KW Chimeric antibody; monoclonal antibody; ME4; antibody engineering;

KW tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;

KW ovary carcinoma; melanoma; cancer; diagnosis; therapy; light chain.

OS Mus sp.

PN US5576184-A.

PD 19-NOV-1996.

PF 06-SEP-1988; US-240624.

PR 08-SEP-1988; US-241744.

PR 13-SEP-1988; US-243739.

PR 04-OCT-1988; US-253002.

PR 19-JUN-1989; US-367841.

PR 21-JUL-1989; US-382768.

PR 06-MAY-1991; US-659401.

PR 27-DEC-1994; US-364001.

PA (XOMA) XOMA CORP.

PI Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;

DR WPI; 97-011249/01.

DR N-PSDB; T43440.

PT Chimeric mouse-human antibodies - recognise a human tumour antigen,

PT used for the treatment and diagnosis of human cancers

PS Example 3; Fig 29; 102pp; English.

CC The light chain variable region (W06215) of mouse monoclonal

CC antibody ME4 is the product of a cDNA clone (T43440) isolated

CC from a ME4 hybridoma cDNA library. MAB ME4 (IgG1) binds to an

CC antigen that is expressed on the surface of human lung, breast,

CC colon and ovary carcinomas and melanomas, but not on most normal
 CC adult tissues. The light chain and heavy chain variable regions
 CC (see also W06216) of ME4 can be linked to human constant regions
 CC and expressed in transformed host cells. Novel mouse-human
 CC chimeric antibodies (see also W06209-14 and W06217-18) can be
 CC produced that have specificity to human tumour antigens for use in
 CC the treatment and diagnosis of human cancer.
 SQ Sequence 128 AA;

Query Match 100.0%; Score 51; DB 19; Length 128;
 Best Local Similarity 100.0%; Pred. No. 5.83e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 ytsrlhs 76
 ||||||
 QY 1 YTSRLHS 7

RESULT 14
 ID R09426 standard; Protein; 128 AA.
 AC R09426; 1993 (first entry)
 DE ME4 Light Chain V Region (mouse).
 KW Monoclonal antibody; chimera; light; heavy; chain; constant;
 KW variable; antigen; diagnosis; cancer; tumour.
 OS Mus musculus.
 PN W09002569-A.
 PD 22-MAR-1990. U03852.
 PF 06-SEP-1989; US-240624.
 PR 06-SEP-1988; US-241744.
 PR 08-SEP-1988; US-243739.
 PR 13-SEP-1988; US-253002.
 PR 04-OCT-1988; US-367641.
 PR 19-JUN-1989; US-382768.
 PR 21-JUL-1989; US-382768.
 PA (ITGE-) INT GENETIC ENG INC.
 PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
 DR WPI: 90-115825/15.
 DR N-PSDB: Q08608.
 PT Chimeric mouse-human antibodies - prepd. using genes coding for
 PT constant human region murine variable region, esp. to 3 tumour
 PT antigen
 PS Claim 13; Page 123 + Fig 29; 173pp; English.
 CC The sequence is used in the prodn. of a chimeric antibody mol.
 CC comprising two light chains and two heavy chains, each having a
 CC constant region (human) and a variable region (murine) having
 CC specificity to an antigen bound by murine monoclonal antibody
 CC (WAB) ME4. The chimeric antibodies can be used for any purpose for
 CC which the original murine MABs can be used, with the advantage that
 CC they are more compatible with the human body. They are esp. used for
 CC the diagnosis and treatment of cancer.
 SQ Sequence 128 AA;

Query Match 100.0%; Score 51; DB 5; Length 128;
 Best Local Similarity 100.0%; Pred. No. 5.83e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 ytsrlhs 76
 ||||||
 QY 1 YTSRLHS 7

RESULT 15
 ID R47207 standard; Protein; 129 AA.
 AC R47207;
 DT 09-AUG-1994 (first entry)
 DE Human/murine IL-1 chimeric antibody VL.
 KW Probe; chimeric; recombinant; antibody; human; interleukin-1; IL-1;
 KW light; L chain; constant; region; variable; mouse; anti-human;
 KW graft; CDR; complementarity determining region; heavy; H;
 KW inflammatory disease; arteriosclerosis; detection;
 KW diffused intravascular coagulation; leukemia.
 OS Synthetic.

FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "Signal peptide"
 FT Protein 21..129
 FT /note= "Mature protein"
 PN W09402627-A.
 PD 03-FEB-1994.
 PF 08-JUL-1993; J00941.
 PR 16-JUL-1992; JP-189248.
 PA (SAKA) OTSUKA PHARM CO LTD.
 PI Hirai Y, Nishida T, Omoto Y, Owens RJ;
 DR WPI: 94-04885/06.
 DR N-PSDB: Q56068.
 PT Mouse/human chimeric antibody against human interleukin-1 - for
 PT treatment of diseases in which production of interleukin-1 is
 PT abnormal, and for diagnostic imaging of interleukin-1 production
 PT sites in vivo
 PS Claim 2; Fig 10; 58pp; Japanese.
 CC The sequences given in R47205-08 represent the light and heavy chain,
 CC variable and constant regions of a chimeric recombinant antibody
 CC against human interleukin-1 (IL-1). The antibody has a light (L)
 CC chain in which the constant region is that of a human antibody and
 CC the variable region is from a mouse anti-human IL-1 antibody or is a
 CC mouse-human graft containing the CDR regions of mouse anti-human IL-1
 CC antibody, and a heavy (H) chain in which the constant region is that
 CC of a human antibody and the variable region is from a mouse anti-human
 CC IL-1 antibody or is a mouse-human graft containing the CDR regions of
 CC mouse anti-human IL-1 antibody. The chimeric antibody is used to
 CC treat diseases in which abnormal amounts of IL-1 are produced, eg.
 CC inflammatory disease, arteriosclerosis, diffused intravascular
 CC coagulation or leukemia. It can also be labelled and used for
 CC diagnostic imaging of IL-1 producing sites in vivo.
 SQ Sequence 129 AA;

Query Match 100.0%; Score 51; DB 9; Length 129;
 Best Local Similarity 100.0%; Pred. No. 5.83e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 ytsrlhs 76
 ||||||
 QY 1 YTSRLHS 7

RESULT 16
 ID R84553 standard; Protein; 131 AA.
 AC R84553;
 DT 02-FEB-1996 (first entry)
 DE MAB SCH94.03 light chain.
 KW Monoclonal antibody; MAB; SCH94.03; hybridoma; central nervous system;
 KW CNS; demyelination; multiple sclerosis; neural disease; therapeutic.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= Leader_peptide
 FT Region 44..54
 FT /label= CDR1
 FT Region 70..76
 FT /label= CDR2
 FT Region 109..117
 FT /label= CDR3
 FT Region 116..128
 FT /label= Joining_region
 FT Region 129..131
 FT /label= C-kappa_region
 PN W09530004-A1.
 PD 09-NOV-1995.
 PF 27-APR-1995; U05262.
 PR 29-APR-1994; US-236520.
 PA (MAYO-) MAYO FOUNDATION.
 PI Miller DJ, Rodriguez M;
 DR WPI: 95-393077/50.
 DR N-PSDB: T05311.
 PT Monoclonal antibodies which stimulate central nervous system

PT re-myelination - are produced by hybridoma ATCC CRL 11627, for
PT treating multiple sclerosis, and viral or post-neural diseases of
PT the CNS.
PS Disclosure; Page 36-37; 63pp; English.
CC Hybridoma ATCC CRL 11627 was obtained from a SJL/J mouse injected with
CC spinal cord homogenate from a mammal uninfected with any
CC demyelinating disease. The hybridoma produced a monoclonal antibody
CC (SCH94.03) useful in promoting CNS remyelination. The SCH94.03
CC light chain amino acid sequence is given in R84553.
SQ Sequence 131 AA;

Query Match 100.0%; Score 51; DB 14; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.83e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 70 ytsrlhs 76
|||||||
QY 1 YTSRLHS 7

RESULT 17

ID R44226 standard; protein; 268 AA.
AC R44226;
DT 10-JUN-1994 (first entry)
DE Chimeric Ig superfamily protein analogue R19(D1.3).
KW CHI-protein; immunoglobulin superfamily; multivalent antigen binding;
KW engineered fusion protein; beta-barrel domain; chimaeric;
KW complementarity determining region; cell imaging; targeting.
OS Synthetic.

FH Key Location/Qualifiers

FT Region 1..30
FT /label= H_FR1
FT /note= "Heavy chain framework region from R19.9"
FT Region 31..35
FT /label= H1
FT /note= "Primary CDR loop from R19.9"
FT Region 36..39
FT /label= FR2A
FT /note= "Heavy chain framework region from R19.9"
FT Region 40..45
FT /label= H3'
FT /note= "CDR loop spliced into chi-site from D1.3"
FT Region 46..48
FT /label= FR2B
FT /note= "Heavy chain framework region from R19.9"
FT Region 49..65
FT /label= H2
FT /note= "Primary CDR loop from R19.9"
FT Region 66..89
FT /label= H_FR3A
FT /note= "Heavy chain framework region from R19.9"
FT Region 90..92
FT /label= H1'
FT /note= "CDR loop spliced into chi-site from D1.3"
FT Region 93..97
FT /label= H_FR3B
FT /note= "Heavy chain framework region from R19.9"
FT Region 98..112
FT /label= H3
FT /note= "Primary CDR loop from R19.9"
FT Region 113..116
FT /label= H_FR4
FT /note= "Heavy chain framework region from R19.9"
FT Region 117..135
FT /label= H2'
FT /note= "CDR loop spliced into chi-site from D1.3"
FT Region 136..155
FT /note= "bridge/linker"
FT Region 156..178
FT /label= L_FR1
FT /note= "Light chain framework region from R19.9"
FT Region 179..189
FT /label= L1

FT /note= "Primary CDR loop from R19.9"
FT Region 190..193
FT /label= FR2A
FT /note= "Light chain framework region from R19.9"
FT Region 194..199
FT /label= L3'
FT /note= "CDR loop spliced into chi-site from D1.3"
FT Region 200..203
FT /label= FR2B
FT /note= "Light chain framework region from R19.9"
FT Region 204..210
FT /label= L2
FT /note= "Primary CDR loop from R19.9"
FT Region 211..237
FT /label= L_FR3A
FT /note= "Light chain framework region from R19.9"
FT Region 238..241
FT /label= L1'
FT /note= "CDR loop spliced into chi-site from D1.3"
FT Region 242..244
FT /label= FR3B
FT /note= "Light chain framework region from R19.9"
FT Region 245..253
FT /label= L3
FT /note= "Primary CDR loop from R19.9"
FT Region 254..255
FT /label= FR4
FT /note= "Light chain framework region from R19.9"
FT Region 256..268
FT /label= L2'
FT /note= "CDR loop spliced into chi-site from D1.3"
FT W09323537-A.
PD 25-NOV-1993.
PF 07-MAY-1993; U04338.
PA (CREA-) CREATIVE BIOMOLECULES.
PI Huston JS, Keck PC;
DR WPI; 93-386569/48.
PT Chimeric multivalent protein analogues - useful for diagnostic
PT imaging and cytotoxic therapy
PS Example 1; Fig 14; 106pp; English.
CC This sequence is an example of a CHI-protein constructed according
CC to the invention. The novel CHI (Chimeric Immunoglobulin)-proteins
CC are comprised of at least 1 beta-barrel forming domain. The antigen
CC binding sites of the molecule are located in the beta-barrel
CC domain(s). Splice sites for insertion of specific binding sites are
CC located by computer comparisons of homology and structure. Depending
CC on the ligand binding specificity of the chimeric molecules, they
CC can be targeted for imaging, irradiating or delivering cytotoxic
CC substances to specific tissues.
SQ Sequence 268 AA;

Query Match 100.0%; Score 51; DB 8; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.83e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 204 ytsrlhs 210
|||||||
QY 1 YTSRLHS 7

RESULT 18

ID R60206 standard; protein; 302 AA.
AC R60206;
DT 14-MAR-1995 (first entry)
DE Bispecific CD3-L6Fvlg antibody derivative.
KW fusion protein; recombinant bispecific single chain antibody;
KW helical peptide linker; anti-L6 antibody; tumour cell antigen;
KW anti-CD3 antibody; variable region.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= L6_VL_leader

```

FT Region 24..271
FT /label= CD3_VL-VH_fusion
FT Region 134..148
FT /label= (Gly4Ser)3_linker
FT Region 272..274
FT /label= hinge
FT Region 275..302
FT /label= Fv_helical_linker
PN EP-610046-A.
PD 10-AUG-1994. 300692.
PF 31-JAN-1994; US-013420.
PR 01-FEB-1993; US-121054.
PR 13-SEP-1993; US-121054.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PI Bajorth J, Fell PH, Gilliland LK, Hayden MS, Ledbetter JA,
PI Linsley PS;
DR WPI: 94-250885/31.
DR N-PSDB: Q81076.
PT Expression vector encoding bispecific fusion protein - having
PT binding domains for separate targets joined by helical peptide,
PT useful e.g. for diagnosis and treatment
PT Example 1, Fig 11 and Page 29-31, 50pp; English.
PS The VL and VH sequences of the anti-CD3 hybridoma G19-4 were
CC amplified by PCR methods. A gene fusion was constructed from the
CC two amplified domains and a (Gly4Ser)3 linker. The amino
CC terminus of the VL-VH fusion cassette was fused at the Sali site to
CC the L6 light chain variable region leader peptide and the
CC carboxy-terminus was fused directly to the hinge region of the FC
CC domain at the BclI site and/or to a short "helical" peptide linker
CC to construct the bispecific CD3-L6Fvlg antibody derivative. The
CC variable regions for L6 were fused in frame to the opposite end of
CC the helical linker (not included in R60206).
SQ Sequence 302 AA;

Query Match 100.0%; Score 51; DB 10; Length 302;
Best Local Similarity 100.0%; Pred. No. 5.83e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 73 ytsrlhs 79
| | | | | | | |
QY 1 YTSRLHS 7

RESULT 19
ID R99003 standard; Protein; 127 AA.
AC R99003.
DT 10-JAN-1997 (first entry)
DE MAb VU1E6 light chain (specific for human alphav integrins).
KW Monoclonal antibody; MAb; integrin; cell-matrix interaction;
KW tumour; melanoma; glioma; carcinoma; cytokine; interleukin-2; IL-2;
KW imaging; detection; radiolabel.
OS Mus musculus.
FH Key Location/Qualifiers
FT Region 21..43
FT /label= Framework region 1
FT Binding_site 44..54
FT /label= CDR1
FT Region 55..69
FT /label= Framework region 2
FT Binding_site 70..76
FT /label= CDR2
FT Region 77..108
FT /label= Framework region 3
FT Binding_site 109..117
FT /label= CDR3
FT Region 118..127
FT /label= Framework region 4
FT /label= Framework region 4
PN EP-719859-A1.
PD 03-JUL-1996.
PF 06-DEC-1995; 119233.
PR 20-DEC-1994; EP-120165.
PA (MERE) MERCK PATENT GMBH.
PI Adan J, Goodman S, Hahn D, Mitjans F, Piulats J;

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PI Rosell E;
DR WPI: 96-302345/31.
DR N-PSDB: T35050.
PT New human integrin V chain-specific monoclonal antibody - and
PT related DNA and hybridomas, for treatment and diagnostic imaging of
PT tumours, esp melanoma.
PS Claim 8; Figure 17a; 54pp; English.
CC A monoclonal antibody which reacts only with the alphav chain of
CC human alphav integrins; which blocks attachment of alphav integrin
CC bearing cells to integrin substrate; which reverses established cell
CC matrix interactions caused by alphav integrin; which blocks tumour
CC development and which has no cytotoxic activity, may be used to
CC treat tumours, especially melanoma (but also glioma, carcinoma)
CC optionally coupled to a cytokine such as interleukin-2. The
CC monoclonal antibody may also be used for diagnostic imaging of
CC tumours and assessment of tumour growth when conjugated to a
CC radiolabel or a radio opaque-agent.
SQ Sequence 127 AA;

Query Match 90.2%; Score 46; DB 19; Length 127;
Best Local Similarity 85.7%; Pred. No. 2.76e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 70 ytsrlhs 76
| | | | | | | |
QY 1 YTSRLHS 7

Search completed: Tue Mar 3 14:28:25 1998
Job time : 17 secs.

```

W P E R E H

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 3 14:32:15 1998; MasPar time 2.93 Seconds

Tabular output not generated.
72.785 Million cell updates/sec

Title: >US-08-137-117D-118
Description: (1-7) from US08137117D.pgp
Perfect Score: 51
Sequence: 1 YTSRLHS 7

Scoring table:
PAM 150
Gap 15

Searched: 95051 seqs, 30469580 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir53
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unann11 16:unann12 17:unann
18:unrev

Statistics: Mean 20.894; Variance 23.719; scale 0.881

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	51	100.0	93	7	S38564	Ig light chain V reg	2.38e-01
2	51	100.0	107	7	B48677	Ig light chain V-J r	2.38e-01
3	51	100.0	107	7	S69901	Ig kappa light chain	2.38e-01
4	51	100.0	107	7	S69906	Ig kappa light chain	2.38e-01
5	51	100.0	107	7	B28044	Ig kappa chain V reg	2.38e-01
6	51	100.0	107	7	B49026	Ig kappa chain V reg	2.38e-01
7	51	100.0	107	7	A28044	Ig kappa chain V reg	2.38e-01
8	51	100.0	107	7	C48677	Ig light chain V-J r	2.38e-01
9	51	100.0	107	7	D48677	Ig light chain V-J r	2.38e-01
10	51	100.0	108	7	S69902	Ig kappa light chain	2.38e-01
11	51	100.0	108	7	S69903	Ig kappa light chain	2.38e-01
12	51	100.0	108	2	KVMSAR	Ig kappa chain V reg	2.38e-01
13	51	100.0	108	7	S38862	Ig kappa chain V reg	2.38e-01
14	51	100.0	108	7	S69900	Ig kappa light chain	2.38e-01
15	51	100.0	108	7	S19970	Ig kappa chain V reg	2.38e-01
16	51	100.0	109	7	PH0888	Ig light chain V reg	2.38e-01
17	51	100.0	115	7	A53276	Ig kappa chain V reg	2.38e-01
18	51	100.0	115	7	JL0080	Ig light chain precu	2.38e-01
19	51	100.0	122	7	A29380	Ig kappa chain precu	2.38e-01
20	51	100.0	127	7	PH1224	Ig kappa chain precu	2.38e-01

21	51	100.0	128	7	A26406	Ig kappa chain V reg	2.38e-01
22	48	94.1	107	7	A48677	Ig light chain V-J r	1.21e+00
23	48	94.1	470	9	S02068	RNA-directed RNA pol	1.21e+00
24	48	94.1	529	9	A24031	genome polyprotein -	1.21e+00
25	48	94.1	2332	4	GNNY4F	genome polyprotein -	1.21e+00
26	48	94.1	2332	4	GNNYF	genome polyprotein -	1.21e+00
27	48	94.1	2333	4	GNNY2F	genome polyprotein -	1.21e+00
28	46	90.2	126	7	A34904	Ig kappa chain precu	3.44e+00
29	45	88.2	470	9	JN0431	RNA-directed RNA pol	5.75e+00
30	45	88.2	473	18	S53119	RNA-dependent RNA po	5.75e+00
31	45	88.2	2336	9	S37077	genome polyprotein -	5.75e+00
32	44	86.3	105	7	PH0087	Ig kappa chain V reg	9.53e+00
33	44	86.3	178	2	TVRTBM	transforming protein	9.53e+00
34	44	86.3	230	16	S33161	Ig kappa chain - she	9.53e+00
35	44	86.3	502	8	A23547	keratin, type II cyt	9.53e+00
36	43	84.3	847	14	JC4836	alpha-glucuronidase	1.57e+01
37	43	84.3	975	14	S4751	hypothetical protein	1.57e+01
38	42	82.4	107	7	S32186	Ig kappa chain V reg	2.55e+01
39	42	82.4	274	13	S17923	rbcL intron protein	2.55e+01
40	42	82.4	334	12	S19843	iron-uptake system c	2.55e+01
41	42	82.4	721	13	S49789	hypothetical protein	2.55e+01
42	42	82.4	747	13	S69557	hypothetical protein	2.55e+01
43	42	82.4	787	13	S56268	hypothetical protein	2.55e+01
44	42	82.4	961	15	A53380	faciogenital dysplas	2.55e+01
45	41	80.4	111	7	E38740	Ig kappa chain V reg	4.13e+01

ALIGNMENTS

RESULT	1
ENTRY	S38564
TITLE	Ig light chain V region (ASWU1) - mouse (fragment)
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-May-1997
ACCESSIONS	S38564
REFERENCE	S38559
#authors	Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
#submission	Submitted to the EMBL Data Library, September 1993
#description	Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s Mice.
#accession	S38564
#status	Preliminary
#molecule_type	mRNA
#residues	1-93
#label	MON
#cross-references	EMBL:X75105
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS	immunoglobulin
SUMMARY	#length 93 #checksum 1511

Query Match 100.0%; Score 51; DB 7; Length 93;
Best Local Similarity 100.0%; Pred No. 2.38e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 ytsrlhs 56
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Qy 1 YTSRLHS 7

RESULT	2
ENTRY	B48677
TITLE	Ig light chain V-J region (44.1) - mouse (fragment)
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	19-May-1994 #sequence_revision 19-May-1994 #text_change 16-Aug-1996

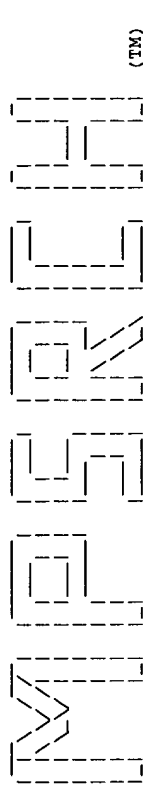
ACCESSIONS
REFERENCE
#authors
#journal
#title
Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb,
P.; Brown, A.; Hasemann, C.A.; Capra, J.D.; Meek, K.
Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9508-9512
Molecular characterization of monoclonal CRI-A-positive
anti-arsonate antibodies derived from idiotype-negative
mice bearing a light chain polymorphism.

TITLE	Ig light chain V-J region (24) - mouse (fragment)		
ORGANISM	#formal_name Mus musculus #common_name house mouse		
DATE	19-May-1994 #sequence_revision 19-May-1994 #text_change 16-Aug-1996		
ACCESSIONS	D48677		
REFERENCE	Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C.A.; Capra, J.D.; Meek, K.		
#authors			
#journal	Molecular. Acad. Sci. U.S.A. (1993) 90:9508-9512		
#title	Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibodies derived from idiotypic-negative mice bearing a light chain polymorphism.		
#accession	D48677		
#status	preliminary; not compared with conceptual translation		
#molecule_type	mRNA		
#residues	1-107 #label TAS		
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology		
KEYWORDS	immunoglobulin		
SUMMARY	#length 107 #checksum 7155		
Query Match	100.0%; Score 51; DB 7; Length 107;		
Best Local Similarity	100.0%; Pred. No. 2.38e-01;		
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	50 ytsrlhs 56		
Qy	1 YTSRLHS 7		
RESULT	10		
ENTRY	S69902 #type complete		
TITLE	Ig kappa light chain (clone KL2.28) - mouse		
ORGANISM	#formal_name Mus musculus #common_name house mouse		
DATE	14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-May-1997		
ACCESSIONS	S69902		
REFERENCE	S69900		
#authors	Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.		
#journal	Immunology (1992) 75:116-121		
#title	B-cell proliferation initiated by Ia cross-linking and sustained by interleukins leads to class switching but not somatic mutation in vitro.		
#accession	S69902		
#status	preliminary; translation not shown		
#molecule_type	DNA		
#residues	1-108 #label WYS		
#cross-references	EMBL:X55043		
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology		
SUMMARY	#length 108 #molecular-weight 11895 #checksum 1228		
Query Match	100.0%; Score 51; DB 7; Length 108;		
Best Local Similarity	100.0%; Pred. No. 2.38e-01;		
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	50 ytsrlhs 56		
Qy	1 YTSRLHS 7		
RESULT	11		
ENTRY	S69903 #type complete		
TITLE	Ig kappa light chain (clone KL2.29) - mouse		
ORGANISM	#formal_name Mus musculus #common_name house mouse		
DATE	14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-May-1997		
ACCESSIONS	S69903		
REFERENCE	S69900		
#authors	Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.		
#journal	Immunology (1992) 75:116-121		
#title	B-cell proliferation initiated by Ia cross-linking and sustained by interleukins leads to class switching but not somatic mutation in vitro.		
#accession	S69903		

#description	Production and cloning of TMV-specific monoclonal antibodies.
#accession	S38862
#status	preliminary
#molecule_type	mRNA
#residues	1-108 #label FIS
#cross-references	EMBL:X75954
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS	heterotetramer; immunoglobulin
SUMMARY	#length 108 #molecular-weight 11865 #checksum 1422
Query Match	100.0%; Score 51; DB 7; Length 108;
Best Local Similarity	100.0%; Pred. No. 2.38e-01;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	50 ytsrlhs 56
QY	1 YTSRLHS 7
RESULT	14
ENTRY	S69900 #type complete
TITLE	Ig kappa light chain (clone KL2.18) - mouse
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-May-1997
ACCESSIONS	S69900
REFERENCE	S69900
#authors	Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
#journal	Immunology (1992) 75:116-121
#title	B-cell proliferation initiated by Ia cross-linking and sustained by interleukins leads to class switching but not somatic mutation in vitro.
#accession	S69900
##status	preliminary; translation not shown
##molecule_type	DNA
##residues	1-108 #label WYS
##cross-references	EMBL:X55041
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY	#length 108 #molecular-weight 11954 #checksum 1768
Query Match	100.0%; Score 51; DB 7; Length 108;
Best Local Similarity	100.0%; Pred. No. 2.38e-01;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	50 ytsrlhs 56
QY	1 YTSRLHS 7
RESULT	15
ENTRY	S19970 #type fragment
TITLE	Ig kappa chain V region (M-Ti51) - mouse (fragment)
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 16-Aug-1996
ACCESSIONS	S19970
REFERENCE	S19970
#authors	Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
#submission	submitted to the EMBL Data Library, March 1992
#description	Structural characterization of CD4 mAb.
#accession	S19970
##status	preliminary
##molecule_type	mRNA
##residues	1-108 #label WEI
##cross-references	EMBL:X65095
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS	heterotetramer; immunoglobulin
SUMMARY	#length 108 #checksum 2135
Query Match	100.0%; Score 51; DB 7; Length 108;
Best Local Similarity	100.0%; Pred. No. 2.38e-01;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	50 ytsrlhs 56 QY 1 YTSRLHS 7
RESULT 16	
ENTRY	PH0888 #type fragment
TITLE	Ig light chain V region (anti-CD3) - mouse (fragment)
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996
ACCESSIONS	PH0888
REFERENCE	PH0885
#authors	Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann, M.; Carter, P.
#journal	J. Exp. Med. (1992) 175:217-225
#title	Development of humanized bispecific antibodies reactive with cytotoxic lymphocytes and tumor cells overexpressing the HER2 protooncogene.
#cross-references	MUID:92113462
#accession	PH0888
#molecule_type	mRNA
#residues	1-109 ##label SHA
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS	immunoglobulin
SUMMARY	#length 109 #checksum 4838
Query Match	100.0%; Score 51; DB 7; Length 109;
Best Local Similarity	100.0%; Pred.No. 2.38e-01;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	50 ytsrlhs 56
QY	1 YTSRLHS 7
RESULT 17	
ENTRY	A53276 #type complete
TITLE	Ig kappa chain V region - mouse
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	02-May-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
ACCESSIONS	A53276
REFERENCE	A53276
#authors	Kim, S.O.; Sanz, I.; Williams, C.; Capra, J.D.; Gottlieb, P.D.
#journal	Immunogenetics (1991) 34:231-241
#title	Polymorphism in V kappa 10 genes encoding L chains of antibodies bearing the Ars-A and A48 cross-reactive idiotypes.
#cross-references	MUID:92010099
#accession	A53276
#status	preliminary
#molecule_type	DNA
#residues	1-115 ##label KIM
#cross-references	NCBIN:62777; NCBIP:62780
#experimental_source	Av1 strain
#note	sequence extracted from NCBI backbone
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS	heterotetramer; immunoglobulin
SUMMARY	#length 115 #molecular_weight 12681 #checksum 7342
Query Match	100.0%; Score 51; DB 7; Length 115;
Best Local Similarity	100.0%; Pred.No. 2.38e-01;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	70 ytsrlhs 76
QY	1 YTSRLHS 7
RESULT 18	
ENTRY	JL0080 #type fragment
TITLE	Ig light chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment)
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996
ACCESSIONS	JL0080
REFERENCE	JL0076
#authors	Karttinen, M.; Rocca-Serra, J.; Maekela, O.
#journal	Mol. Immunol. (1988) 25:859-865
#title	Combinatorial association of V genes: one VH gene codes for three non-cross-reactive monoclonal antibodies each specific for a different antigen (phoxazolone, NP or GAT).
#cross-references	MUID:89096973
#accession	JL0080
#molecule_type	mRNA
#residues	1-115 ##label KAA
#note	the authors translated the codon AGG for residue 30 as Ser
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS	immunoglobulin
FEATURE	1-6
7-115	#domain signal sequence (fragment) #status predicted
30-40	#product Ig light chain #status predicted #label MAT\
56-62	#region complementarity-determining 1\
SUMMARY	#length 115 #checksum 7375
Query Match	100.0%; Score 51; DB 7; Length 115;
Best Local Similarity	100.0%; Pred.No. 2.38e-01;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	56 ytsrlhs 62
QY	1 YTSRLHS 7
RESULT 19	
ENTRY	A29380 #type fragment
TITLE	Ig kappa chain precursor V region (AC-1001) - mouse
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Aug-1996
ACCESSIONS	A29380
REFERENCE	A92612
#authors	Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
#journal	J. Biol. Chem. (1987) 262:13379-13583
#title	Nucleotide and translated amino acid sequences of cDNA coding for the variable regions of the light and heavy chains of mouse hybridoma antibodies to blood group A and B substances.
#cross-references	MUID:88007582
#accession	A29380
#molecule_type	mRNA
#residues	1-122 ##label CHE
#note	the authors translated the codon TTC for residue 1 as Leu
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS	heterotetramer; immunoglobulin
SUMMARY	#length 122 #checksum 9064
Query Match	100.0%; Score 51; DB 7; Length 122;
Best Local Similarity	100.0%; Pred.No. 2.38e-01;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	64 ytsrlhs 70
QY	1 YTSRLHS 7
RESULT 20	
ENTRY	PH1224 #type fragment
TITLE	Ig light chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment)
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996
ACCESSIONS	JL0080
REFERENCE	JL0076
#authors	Karttinen, M.; Rocca-Serra, J.; Maekela, O.
#journal	Mol. Immunol. (1988) 25:859-865
#title	Combinatorial association of V genes: one VH gene codes for three non-cross-reactive monoclonal antibodies each specific for a different antigen (phoxazolone, NP or GAT).
#cross-references	MUID:89096973
#accession	JL0080
#molecule_type	mRNA
#residues	1-115 ##label KAA
#note	the authors translated the codon AGG for residue 30 as Ser
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS	immunoglobulin
FEATURE	1-6
7-115	#domain signal sequence (fragment) #status predicted
30-40	#product Ig light chain #status predicted #label MAT\
56-62	#region complementarity-determining 1\
SUMMARY	#length 115 #checksum 7375
Query Match	100.0%; Score 51; DB 7; Length 115;
Best Local Similarity	100.0%; Pred.No. 2.38e-01;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	56 ytsrlhs 62
QY	1 YTSRLHS 7
RESULT 19	
ENTRY	A29380 #type fragment
TITLE	Ig kappa chain precursor V region (AC-1001) - mouse
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Aug-1996
ACCESSIONS	A29380
REFERENCE	A92612
#authors	Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
#journal	J. Biol. Chem. (1987) 262:13379-13583
#title	Nucleotide and translated amino acid sequences of cDNA coding for the variable regions of

Search completed: Tue Mar 3 14:32:31 1998
Job time : 16 secs.



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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 3 11:20:10 1998; MasPar time 1.99 Seconds
Tabular output not generated. 74.523 Million cell updates/sec

Title: >US-08-137-117D-118
Description: (1-7) from US08137117D.pep
Perfect Score: 51
Sequence: 1 YTSRLHS 7

Scoring table: PAM 150
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 21.579; Variance 20.158; scale 1.070

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	51	100.0	108	5	IG KAPPA CHAIN V-V RE	3.04e-02
2	51	100.0	108	5	IG KAPPA CHAIN V-V RE	3.04e-02
3	51	100.0	108	5	IG KAPPA CHAIN V-V RE	3.04e-02
4	51	100.0	108	5	IG KAPPA CHAIN V-V RE	3.04e-02
5	51	100.0	108	5	IG KAPPA CHAIN V-V RE	3.04e-02
6	51	100.0	108	5	IG KAPPA CHAIN V-V RE	3.04e-02
7	48	94.1	861	7	IG KAPPA CHAIN V-V RE	3.04e-02
8	48	94.1	2332	7	IG KAPPA CHAIN V-V RE	3.04e-02
9	48	94.1	2332	7	IG KAPPA CHAIN V-V RE	3.04e-02
10	48	94.1	2332	7	IG KAPPA CHAIN V-V RE	3.04e-02
11	45	88.2	2336	6	IG KAPPA CHAIN V-V RE	3.04e-02
12	44	86.3	178	6	IG KAPPA CHAIN V-V RE	3.04e-02
13	44	86.3	502	5	IG KAPPA CHAIN V-V RE	3.04e-02
14	43	84.3	942	3	IG KAPPA CHAIN V-V RE	3.04e-02
15	42	82.4	334	3	IG KAPPA CHAIN V-V RE	3.04e-02
16	42	82.4	552	10	IG KAPPA CHAIN V-V RE	3.04e-02
17	42	82.4	721	11	IG KAPPA CHAIN V-V RE	3.04e-02
18	42	82.4	787	11	IG KAPPA CHAIN V-V RE	3.04e-02
19	42	82.4	960	3	IG KAPPA CHAIN V-V RE	3.04e-02
20	42	82.4	961	3	IG KAPPA CHAIN V-V RE	3.04e-02
21	41	80.4	108	5	IG KAPPA CHAIN V-V RE	3.04e-02
22	41	80.4	226	6	IG KAPPA CHAIN V-V RE	3.04e-02

23	41	80.4	348	1	AROH_ECOLI	PHOSPHO-2-DEHYDRO-3-D	1.28e+01
24	41	80.4	425	4	FTSA_HAEIN	CELL DIVISION PROTEIN	1.28e+01
25	41	80.4	665	7	NUC2_SCHPO	NUCLEAR SCAFFOLD-LIKE	1.28e+01
26	40	78.4	210	7	ORAS5_DROME	PUTATIVE ODORANT-BIND	2.21e+01
27	40	78.4	323	9	SOPB_ECOLI	SOPB PROTEIN (PROTEIN	2.21e+01
28	40	78.4	536	3	DIT1_YEAST	SPORE WALL MATURATION	2.21e+01
29	40	78.4	593	8	PTN9_HUMAN	PROTEIN-TYROSINE PHOS	2.21e+01
30	40	78.4	603	7	PRIM_BACSU	DNA PRIMASE (EC 2.7.7	2.21e+01
31	40	78.4	706	1	BCL6_HUMAN	B-CELL LYMPHOMA 6 PRO	2.21e+01
32	40	78.4	707	1	BCL6_MOUSE	B-CELL LYMPHOMA 6 PRO	2.21e+01
33	40	78.4	798	4	HEPA_HCMVA	DNA HELICASE/PRIMASE	2.21e+01
34	40	78.4	1249	9	TPP2_HUMAN	TRIPETIDYL-PEPTIDASE	2.21e+01
35	40	78.4	1942	11	YY05_HUMAN	HYPOTHETICAL MYELOID	2.21e+01
36	39	76.5	152	10	VE1_FPVL	REPLICATION PROTEIN E	3.77e+01
37	39	76.5	309	3	ER25_YEAST	C-4 STEROL METHYL OXI	3.77e+01
38	39	76.5	323	8	R8SC_BACSU	RIBOSE TRANSPORT SYST	3.77e+01
39	39	76.5	335	8	RPOA_FINTH	RNA-DIRECTED RNA POLY	3.77e+01
40	39	76.5	805	10	UBP5_YEAST	UBIQUITIN CARBOXYL-TE	3.77e+01
41	39	76.5	839	6	NI96_YEAST	96 KD NUCLEOPORIN-INT	3.77e+01
42	39	76.5	932	10	VGLB_HSVBC	GLYCOPROTEIN I PRECUR	3.77e+01
43	39	76.5	966	10	VIA_BBMV	1A PROTEIN (CONTAINS	3.77e+01
44	39	76.5	1639	6	LMG1_DROME	LAMININ GAMMA-1 CHAIN	3.77e+01
45	39	76.5	2505	3	FAS_RAT	FATTY ACID SYNTHASE (3.77e+01

ALIGNMENTS

RESULT 1	STANDARD;	PRT;	108 AA.
ID KV5M_MOUSE			
AC P01646;			
DT 21-JUL-1986 (REL. 01, CREATED)			
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)			
DE IG KAPPA CHAIN V-V REGION (HP 123E6).			
OS MUS MUSCULUS (MOUSE).			
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC EUTHERIA; RODENTIA.			
RN [1]			
RP SEQUENCE.			
RC STRAIN-A/J;			
RA MEDLINE; 82150934.			
RA SIEGELMAN M., CAPRA J.D.;			
RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).			
CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.			
DR PIR: A01927; KVMAR.			
DR HSSP: P01607; IFAI.			
KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.			
FT DOMAIN 1 23			
FT DOMAIN 24 34			
FT DOMAIN 35 49			
FT DOMAIN 50 56			
FT DOMAIN 57 88			
FT DOMAIN 89 97			
FT DOMAIN 98 108			
FT DISULFID 23 88			
FT NON_TER 108 108			
SQ SEQUENCE 108 AA; 11989 MW; 2388BB67 CRC32;			
Query Match 100.0%; Score 51; DB 5; Length 108;			
Best Local Similarity 100.0%; Pred. No. 3.04e-02;			
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db 50 ytsrlhs 56			
Qy 1 YTSRLHS 7			
RESULT 2	STANDARD;	PRT;	108 AA.
ID KV5N_MOUSE			
AC P01647;			
DT 21-JUL-1986 (REL. 01, CREATED)			
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)			

DE IG KAPPA CHAIN V-V REGION (HP 124E1).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE; 82150934.
 RA SIEGELMAN M., CAPRA J.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
 CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR; A01927; KVSAR.
 DR HSP; P01607; 1FAI.
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11965 MW; 84754175 CRC32;

Query Match 100.0%; Score 51; DB 5; Length 108;

Best Local Similarity 100.0%; Pred. No. 3.04e-02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 ytsrlhs 56
 QY 1 YTSRLHS 7

RESULT 3
 ID KV5L_MOUSE STANDARD; PRT; 108 AA.
 AC P01645;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-V REGION (HP 93G7).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE; 82150934.
 RA SIEGELMAN M., CAPRA J.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
 CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR; A01927; KVSAR.
 DR HSP; P01607; 1FAI.
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11954 MW; A203E130 CRC32;

Query Match 100.0%; Score 51; DB 5; Length 108;

Best Local Similarity 100.0%; Pred. No. 3.04e-02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 ytsrlhs 56
 QY 1 YTSRLHS 7

RESULT 4
 ID KV5K_MOUSE STANDARD; PRT; 108 AA.
 AC P01644;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-V REGION (HP R16.7).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE; 82150934.
 RA SIEGELMAN M., CAPRA J.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
 CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR; A01927; KVSAR.
 DR HSP; P01607; 1FAI.
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11910 MW; 64A62905 CRC32;

Query Match 100.0%; Score 51; DB 5; Length 108;

Best Local Similarity 100.0%; Pred. No. 3.04e-02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 ytsrlhs 56
 QY 1 YTSRLHS 7

RESULT 5
 ID KV5O_MOUSE STANDARD; PRT; 108 AA.
 AC P01648;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-V REGION (HP 91A3).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE; 82150934.
 RA SIEGELMAN M., CAPRA J.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
 CC -I- ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR; A01927; KVSAR.
 DR HSP; P01607; 1FAI.
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11961 MW; 5B067780 CRC32;

Query Match

100.0%; Score 51; DB 5; Length 108;

Best Local Similarity 100.0%; Pred. No. 3.04e-02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 ytsrlhs 56
| | | | | |
Qy 1 YTSRLHS 7

RESULT 6
ID KVSU_MOUSE STANDARD; PRT; 108 AA.
AC P04946;
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-V REGION (NQ5-89.4).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83271467
RA KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;
RL NATURE 304:320-324(1983).
CC -1- ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
DR EMBL; K00745; G196455; -.
DR HSP; P01607; 1PAI.
KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11866 MW; D396FLI42 CRC32;

Query Match 100.0%; Score 51; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.04e-02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 ytsrlhs 56
| | | | | |
Qy 1 YTSRLHS 7

RESULT 7
ID POLG_FMDVS STANDARD; PRT; 861 AA.
AC P03311;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GENOME POLYPROTEIN (COAT PROTEINS VP3, VP1; CORE PROTEIN P52, PROTEASE
DE (EC 3.4.22.-); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48)) (FRAGMENTS).
OS FOOT-AND-MOUTH DISEASE VIRUS (STRAIN C1-SANTA PAU [C-58]) (APHTHOVIRUS
OS C.).
OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; APHTHOVIRUSES.
RN [1]
RP SEQUENCE OF 1-332 FROM N.A.
RX MEDLINE; 84005890.
RA VILLANUEVA N., DAVILA M., ORTIN J., DOMINGO E.;
RL GENE 23:185-194(1983).
RN [2]
RP SEQUENCE OF 333-861 FROM N.A.
RX MEDLINE; 85286357.
RA MARTINEZ-SALAS E., ORTIN J., DOMINGO E.;
RL GENE 35:55-61(1985).
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.

Query Match 100.0%; Score 51; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.04e-02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 ytsrlhs 56
| | | | | |
Qy 1 YTSRLHS 7

RESULT 7
ID POLG_FMDVS STANDARD; PRT; 861 AA.
AC P03311;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GENOME POLYPROTEIN (COAT PROTEINS VP3, VP1; CORE PROTEIN P52, PROTEASE
DE (EC 3.4.22.-); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48)) (FRAGMENTS).
OS FOOT-AND-MOUTH DISEASE VIRUS (STRAIN C1-SANTA PAU [C-58]) (APHTHOVIRUS
OS C.).
OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; APHTHOVIRUSES.
RN [1]
RP SEQUENCE OF 1-332 FROM N.A.
RX MEDLINE; 84005890.
RA VILLANUEVA N., DAVILA M., ORTIN J., DOMINGO E.;
RL GENE 23:185-194(1983).
RN [2]
RP SEQUENCE OF 333-861 FROM N.A.
RX MEDLINE; 85286357.
RA MARTINEZ-SALAS E., ORTIN J., DOMINGO E.;
RL GENE 35:55-61(1985).
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.

DR EMBL; M11027; G210477; -.
DR PIR; A03913; A03913.
DR PIR; A24031; A24031.
DR HSP; P13899; 1FMD.
KW POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW HYDROLASE; THIOL PROTEASE.
FT NON_TER 1 1
FT CHAIN <1 46 COAT PROTEIN VP3.
FT CHAIN 47 254 COAT PROTEIN VP1.
FT CHAIN 255 332 COAT PROTEIN P52.
FT NON_CONS 332 333
FT CHAIN <333 391 PROTEASE.
FT CHAIN 392 861 RNA-DEPENDENT RNA POLYMERASE.
SQ SEQUENCE 861 AA; 95554 MW; 1C8C4098 CRC32;

Query Match 94.1%; Score 48; DB 7; Length 861;
Best Local Similarity 85.7%; Pred. No. 2.05e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 472 ytsrlhs 478
| | | | | |
Qy 1 YTSRLHS 7

RESULT 8
ID POLG_FMDVO STANDARD; PRT; 2332 AA.
AC P03305;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GENOME POLYPROTEIN (NONSTRUCTURAL PROTEIN P20A; COAT PROTEINS VP1 TO
DE VP4; CORE PROTEINS P12, P34, P14; GENOME-LINKED PROTEIN VPG; PROTEASE
DE (EC 3.4.22.-); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48)).
OS FOOT-AND-MOUTH DISEASE VIRUS (STRAINS OIK AND OLBES) (APHTHOVIRUS O).
OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; APHTHOVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-OIK;
RX MEDLINE; 84297249.
RA FORSS S., STREBEL K., BECK E., SCHALLER H.;
RL NUCLEIC ACIDS RES. 12:6587-6601(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-OIBFS;
RX MEDLINE; 83143292.
RA MAKOFF A.J., PAYNTER C.A., ROWLANDS D.J., BOOTHROYD J.C.;
RL NUCLEIC ACIDS RES. 10:8285-8295(1982).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE; 89143740.
RA ACHARYA R., FRY E., STUART D., FOX G., ROWLANDS D., BROWN F.;
RL NATURE 337:709-716(1989).
CC -1- THE STRAIN OIK SEQUENCE IS SHOWN.
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- THE COAT PROTEIN VP1 CONTAINS THE MAIN ANTIGENIC DETERMINANTS OF
CC THE VIRION; THEREFORE, CHANGES IN ITS SEQUENCE MUST BE
CC RESPONSIBLE FOR THE HIGH ANTIGENIC VARIABILITY OF THE VIRUS.
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS.
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.

DR EMBL; X00871; G61078; -.
DR EMBL; J02185; G210436; -.
DR PIR; A03907; GNNYF.
DR HSP; P08544; 1BBT.
KW POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW HYDROLASE; THIOL PROTEASE; MYRISTOLATION.
FT CHAIN 1 201 NONSTRUCTURAL PROTEIN P20A.
FT CHAIN 202 286 COAT PROTEIN VP4.
FT CHAIN 287 504 COAT PROTEIN VP2.
FT CHAIN 505 724 COAT PROTEIN VP3.
FT CHAIN 725 937 COAT PROTEIN VP1.
FT CHAIN 938 1107 CORE PROTEIN P12.

FT CHAIN 1108 1425 CORE PROTEIN P34.
FT CHAIN 1426 1578 CORE PROTEIN P14.
FT CHAIN 1579 1649 GENOME-LINKED PROTEIN VPG.
FT CHAIN 1649 1649 PROTEASE.
FT CHAIN 1650 1862 RNA-DIRECTED RNA POLYMERASE.
FT CHAIN 1863 2332 MYRISTATE.
FT LIPID 202 202 INTERCHAIN (IN VP3 DIMER).
FT DISULFID 511 511 IN VP2-VP1 DIMER.
FT DISULFID 406 858 I -> V (IN STRAIN OIBFS).
FT VARIANT 780 780 G -> R (IN STRAIN OIBFS).
FT VARIANT 808 808 N -> S (IN STRAIN OIBFS).
FT VARIANT 861 861
SQ SEQUENCE 2332 AA; 258924 MW; 251F5647 CRC32;

Query Match 94.1%; Score 48; DB 7; Length 2332;

Best Local Similarity 85.7%; Pred. No. 2.05e-01; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1943 yasrlhs 1949
1:|||||
QY 1 YTSRLHS 7

RESULT 9
ID POLG_FMDVA STANDARD; PRT; 2332 AA.

DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DE GENOME POLYPROTEIN (NONSTRUCTURAL PROTEIN P20A; COAT PROTEINS VP1 TO
DE VP4; CORE PROTEINS X, P14, P41, P19; GENOME-LINKED PROTEINS VPG1 TO
DE VP3; PICORNAIN 3C (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED
DE RNA POLYMERASE (EC 2.7.7.48)).
OS FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A12) (APHTHOVIRUS A).
OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; APHTHOVIRUSES.
RN [1]
RX MEDLINE; 85211015.
RA ROBERTSON B.H., GRUBMAN M.J., WEDDELL G.N., MOORE D.M., WELSH J.D.,
RA FISCHER T., DOWENKO D.J., YANSURA D.G., SMALL B., KLEID D.G.;
RA J. VIROL. 54:651-660(1985).
[2]
RN SEQUENCE OF 1863-2332 FROM N.A.
RX MEDLINE; 83225613.
RA ROBERTSON B.H., MORGAN D.O., MOORE D.M., GRUBMAN M.J., CARD J.,
RA FISCHER T., WEDDELL G.N., DOWENKO D.J., YANSURA D.G.;
RA VIROLOGY 126:614-623(1983).
[3]
RN SEQUENCE OF 715-955 FROM N.A.
RX MEDLINE; 82061853.
RA KLEID D.G., YANSURA D.G., SMALL B., DOWENKO D.J., MOORE D.M.,
RA GRUBMAN M.J., MCKERCHER P.D., MORGAN D.O., ROBERTSON B.H.,
RA BACHRACH H.L.;
RA SCIENCE 214:1125-1129(1981).
CC -1- PTM: SPECIFIC ENZYMIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.

DR EMBL; M10975; G210307; -.
DR EMBL; M10975; E807; -.
DR EMBL; J02187; G210548; -.
DR PIR; A25794; GNNY4F.
DR HSP; P08544; 1BBT.
KW POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW HYDROLASE; THIOL PROTEASE; MYRISTYLATION.
FT CHAIN 1 200 NONSTRUCTURAL PROTEIN P20A.
FT CHAIN 201 285 COAT PROTEIN VP4.
FT CHAIN 286 503 COAT PROTEIN VP2.
FT CHAIN 504 723 COAT PROTEIN VP3.
FT CHAIN 724 937 COAT PROTEIN VP1.
FT CHAIN 938 953 CORE PROTEIN X.
FT CHAIN 954 1107 CORE PROTEIN P14.
FT CHAIN 1108 1425 CORE PROTEIN P41.

FT CHAIN 1426 1578 CORE PROTEIN P19.
FT CHAIN 1579 1601 GENOME-LINKED PROTEIN VPG1.
FT CHAIN 1602 1625 GENOME-LINKED PROTEIN VPG2.
FT CHAIN 1626 1649 GENOME-LINKED PROTEIN VPG3.
FT CHAIN 1650 1862 PROTEASE.
FT CHAIN 1863 2332 RNA-DIRECTED RNA POLYMERASE.
FT LIPID 201 201 MYRISTATE.
SQ SEQUENCE 2332 AA; 259408 MW; BDF68BA5 CRC32;

Query Match 94.1%; Score 48; DB 7; Length 2332;

Best Local Similarity 85.7%; Pred. No. 2.05e-01; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1943 yasrlhs 1949
1:|||||
QY 1 YTSRLHS 7

RESULT 10
ID POLG_FMDV1 STANDARD; PRT; 2333 AA.

AC P03306;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DE GENOME POLYPROTEIN (NONSTRUCTURAL PROTEIN P20A; COAT PROTEINS VP1 TO
DE VP4; CORE PROTEIN P52; GENOME-LINKED PROTEINS VPG1 TO VPG3; PICORNAIN
DE 3C (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE
DE (EC 2.7.7.48)).
OS FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A10-61) (APHTHOVIRUS A).
OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; APHTHOVIRUSES.
RN [1]
RX MEDLINE; 84169547.
RA CARROLL A.R., ROWLANDS D.J., CLARKE B.E.;
RA NUCLEIC ACIDS RES. 12:2461-2472(1984).
[2]
RN SEQUENCE OF 115-1048 FROM N.A.
RX MEDLINE; 82211814.
RA BOOTHROYD J.C., HARRIS T.J.R., ROWLANDS D.J., LOWE P.A.;
RA GENE 17:153-161(1982).
CC -1- PTM: SPECIFIC ENZYMIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.

DR EMBL; V01130; G61049; -.
DR EMBL; X00429; G61064; -.
DR PIR; A03908; GNNY2F.
DR HSP; P08544; 1BBT.
KW POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW HYDROLASE; THIOL PROTEASE; MYRISTYLATION.
FT CHAIN 1 201 NONSTRUCTURAL PROTEIN P20A.
FT CHAIN 202 286 COAT PROTEIN VP4.
FT CHAIN 287 504 COAT PROTEIN VP2.
FT CHAIN 505 725 COAT PROTEIN VP3.
FT CHAIN 726 937 COAT PROTEIN VP1.
FT CHAIN 938 1578 CORE PROTEIN P52.
FT CHAIN 1579 1601 GENOME-LINKED PROTEIN VPG1.
FT CHAIN 1602 1625 GENOME-LINKED PROTEIN VPG2.
FT CHAIN 1626 1649 GENOME-LINKED PROTEIN VPG3.
FT CHAIN 1650 1863 PROTEASE P20B.
FT CHAIN 1864 2333 RNA-DIRECTED RNA POLYMERASE P56A.
FT LIPID 202 202 MYRISTATE.
FT CONFLICT 395 396 S -> C (IN REF. 2).
FT CONFLICT 632 632 P -> L (IN REF. 2).
SQ SEQUENCE 2333 AA; 259645 MW; 7BF32432 CRC32;

Query Match 94.1%; Score 48; DB 7; Length 2333;

Best Local Similarity 85.7%; Pred. No. 2.05e-01; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1944 yasrlhs 1950
1:|||||

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QY 1 YTSRLHS 7

RESULT 11
ID POLG_FMDVZ STANDARD; PRT: 2336 AA.
AC P49303;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE GENOME POLYPROTEIN (NONSTRUCTURAL PROTEIN P20A; COAT PROTEINS VP1 TO
DE VP4; CORE PROTEINS X, P14, P41, P19; GENOME-LINKED PROTEINS VPGL TO
DE VP3; PICORNAIN 3C (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED
DE RNA POLYMERASE (EC 2.7.7.48)).
OS FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A22/550 AZERBAIJAN 65)
OS (APHTHOVIRUS A).
OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; PICORNAVIRIDAE; APHTHOVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RA SOSNOVTSSEV S.V., ONISCHENKO A.M., PETROV N.A., KALASHNIKOVA T.I.,
RA MANAEVA N.V., DRYGIN V.Y., PERVOZCHIKOVA N.A., VASILENKO S.K.;
RL SUBMITTED (AUG-1993) TO EMBL/GENBANK/DDJ DATA BANKS.
CC -!- PM: SPECIFIC ENZYMIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
DR EMBL: X74812; G357966; -.
KW POLYPROTEIN; COAT PROTEIN; CORE PROTEIN; RNA-DIRECTED RNA POLYMERASE;
KW HYDROLASE; THIOLESTERASE; MYRISTYLATION.
FT CHAIN 1 201 NONSTRUCTURAL PROTEIN P20A.
FT CHAIN 202 286 COAT PROTEIN VP4.
FT CHAIN 287 504 COAT PROTEIN VP2.
FT CHAIN 505 724 COAT PROTEIN VP3.
FT CHAIN 725 938 COAT PROTEIN VP1.
FT CHAIN 939 954 CORE PROTEIN X.
FT CHAIN 955 1108 CORE PROTEIN P14.
FT CHAIN 1109 1426 CORE PROTEIN P41.
FT CHAIN 1427 1579 CORE PROTEIN P19.
FT CHAIN 1580 1602 GENOME-LINKED PROTEIN VPGL.
FT CHAIN 1603 1626 GENOME-LINKED PROTEIN VPGL.
FT CHAIN 1627 1650 GENOME-LINKED PROTEIN VPGL.
FT CHAIN 1651 1863 PROTEASE.
FT CHAIN 1864 2336 RNA-DIRECTED RNA POLYMERASE.
FT LIPID 202 202 MYRISTATE (BY SIMILARITY).
SQ SEQUENCE 2336 AA; 259982 MW; 795073B4 CRC32;

Query Match 88.2%; Score 45; DB 7; Length 2336;
Best Local Similarity 71.4%; Pred. No. 1.28e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1944 yasrlhn 1950
QY 1 YTSRLHS 7

RESULT 12
ID MYCB_RAT STANDARD; PRT: 178 AA.
AC P15063;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE B-MYC TRANSFORMING PROTEIN (FRAGMENT).
OS MYCB.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER, AND BRAIN;
RX MEDLINE; 90082428.
RA ASKER C., STEINITZ M., ANDERSSON K., SUEMEGI J., KLEIN G.,
RA INGVARSSON S.;
RA ONCOGENE 4:1523-1527(1989).

[2]
RN SEQUENCE OF 1-120 FROM N.A.
RP MEDLINE; 89096904.
RA INGVARSSON S., ASKER C., AXELSON H., KLEIN G., SUEMEGI J.;
RL MOL. CELL. BIOL. 8:3168-3174(1988).
DR EMBL; X17455; G55831; -.
DR EMBL; M21133; -. NOT_ANNOTATED_CDS.
DR PIR; A31198; TVRTBM.
DR PIR; A45502; A45502.
DR PROSITE; PS00038; HELIX_LOOP_HELIX.
DR TRANSFAC; T01563; -.
DR TRANSFORMING PROTEIN; NUCLEAR PROTEIN; DNA-BINDING.
FT NON_TER 178 178
SQ SEQUENCE 178 AA; 19463 MW; 8AEBC433 CRC32;

Query Match 86.3%; Score 44; DB 6; Length 178;
Best Local Similarity 83.3%; Pred. No. 2.32e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 160 yasrlh 165
QY 1 YTSRLH 6

RESULT 13
ID K2C8_XENLA STANDARD; PRT: 502 AA.
AC P08776;
DT 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE KERATIN, TYPE II CYTOSKELETAL 8 (CYTOKERATIN 8).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86313601.
RA FRANZ J.K., FRANK W.W.;
RL PROC. NATL. ACAD. SCI. U.S.A. 83:6475-6479(1986).
CC -!- THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFILAMENTAR KERATIN.
CC I (ACIDIC) AND II (NEUTRAL TO BASIC) (40-55 AND 56-70 KILODALTONS,
CC RESPECTIVELY).
CC -!- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
CC KERATIN 8 ASSOCIATES WITH KERATIN 18.
CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED IN THE OOCYTE IN EARLY AND LATE
CC EMBRYONIC STAGES.
CC -!- SIMILARITY: TO ALL OTHER INTERMEDIATE FILAMENT PROTEINS.
DR EMBL; M13811; G214556; -.
DR PIR; A23547; A23547.
DR PROSITE; PS00226; IF.
KW INTERMEDIATE FILAMENT; COILED COIL; HEPTAD REPEAT PATTERN; KERATIN.
FT DOMAIN 1 98 HEAD.
FT DOMAIN 99 406 ROD.
FT DOMAIN 407 502 TAIL.
FT DOMAIN 503 534 COIL 1A.
FT DOMAIN 135 151 LINKER 1.
FT DOMAIN 152 243 COIL 1B.
FT DOMAIN 244 267 LINKER 12.
FT DOMAIN 268 406 COIL 2.
FT SITE 350 STUTTER.
SQ SEQUENCE 502 AA; 55679 MW; 79A4B1D3 CRC32;

Query Match 86.3%; Score 44; DB 5; Length 502;
Best Local Similarity 71.4%; Pred. No. 2.32e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 321 yttirlqs 327
QY 1 YTSRLHS 7

RESULT 14
ID KGDG_HUMAN STANDARD; PRT: 942 AA.
AC P52824;
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DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE DIACYLGLYCEROL KINASE, DELTA (EC 2.7.1.107) (DIGLYCERIDE KINASE)
GN DAGK4.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95331799.
RA PILZ A., SCHAAP D., HUNT D., FITZGIBBON J.;
RL GENOMICS 26:599-601(1995).
CC -1- CATALYTIC ACTIVITY: ATP + 1,2-DIACYLGLYCEROL - ADP +
CC 1,2-DIACYLGLYCEROL 3-PHOSPHATE.
CC -1- SIMILARITY: CONTAINS 3 COPIES OF THE ZINC-DEPENDENT PHORBOL-
CC ESTER AND DAG BINDING DOMAIN.
DR EMBL; L38707; G606757; -.
DR MIN; 601207; -.
KW TRANSFERASE; KINASE; PHORBOL-ESTER BINDING; MULTIGENE FAMILY.
FT DOMAIN 61 108 PHORBOL-ESTER AND DAG BINDING (BY
FT SIMILARITY).
FT DOMAIN 122 168 PHORBOL-ESTER AND DAG BINDING (BY
FT SIMILARITY).
FT DOMAIN 184 234 PHORBOL-ESTER AND DAG BINDING (BY
FT SIMILARITY).
SQ SEQUENCE 942 AA; 101403 MW; 34C318EB CRC32;

Query Match 84.3%; Score 43; DB 5; Length 942;
Best Local Similarity 71.4%; Pred. No. 4.14e+00;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 769 ftsrlhn 775
:|||||
Qy 1 YTSRLHS 7

RESULT 15
ID FEUB_RACSU STANDARD; PRT; 334 AA.
AC P40410;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE IRON-UPTAKE SYSTEM PROTEIN FEUB.
GN FEUB.
OS BACILLUS SUBTILIS.
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BD99 / MS94;
RX MEDLINE; 94281248.
RA QUIRK P.G., GUFFANTI A.A., CLEJAN S., CHENG J., KRULWICH T.A.;
RL BIOCHIM. BIOPHYS. ACTA 1186:27-34(1994).
CC -1- FUNCTION: THIS IS ONE OF THE PROTEINS INVOLVED IN AN IRON- UPTAKE
CC SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE
CC SUBSTRATE ACROSS THE MEMBRANE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER INTEGRAL MEMBRANE PROTEINS INVOLVED IN TONB-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE FECCD
CC SUBFAMILY.
DR EMBL; L19954; G438459; -.
DR SUBTILIST; BG10836; FEUB.
DR PROSITE; PS00402; BPD_TRANS_INN_MEMBER.
KW IRON TRANSPORT; TRANSPORT; TRANSMEMBRANE.
FT TRANSMEM 9 29 POTENTIAL.
FT TRANSMEM 63 83 POTENTIAL.
FT TRANSMEM 91 111 POTENTIAL.
FT TRANSMEM 119 139 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
FT TRANSMEM 191 211 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT TRANSMEM 281 301 POTENTIAL.

FT TRANSMEM 305 325 POTENTIAL.
SQ SEQUENCE 334 AA; 35896 MW; 33B73F26 CRC32;
Query Match 82.4%; Score 42; DB 3; Length 334;
Best Local Similarity 66.7%; Pred. No. 7.32e+00;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 182 ytsrlh 187
:|||||
Qy 1 YTSRLH 6

Search completed: Tue Mar 3 11:20:19 1998
Job time : 9 secs.